

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
 A.; Authors: Yoshihara, H.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A.; Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A.; Reference number: A69580; PMID:9804403 ; PMID:9384377
 A.; Accession: P69735
 A.; Status: nucleic acid sequence not shown; translation not shown
 A.; Molecule type: DNA
 A.; Residues: 1-213 <XUN>
 A.; Cross-references: UNIPARC:UPI000033569; GB:Z99114; PIDN:CR
 A.; Experimental source: strain 168
 C; Genetics:
 A; Gene: xynA
 A; Map position: 175 degrees
 C; Function: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
 A; Pathway: xylan degradation
 C; Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C; Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
 F; 1-28/Domain: signal sequence #status predicted <SIG>
 F; 29-213/Domain: endo-1,4-beta-xylanase A #status experimental <MAT>
 F; 31-213/Domain: endo-1,4-beta-xylanase homology <XYL>
 F; 106/200/Active site: Glu #status experimental
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 Query Match 99 7%; Score 1168; DB 1; Length 213;
 Best Local Similarity 99 5%; Pred. No. 3.9e-80;
 Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MFKFKNFKLFLGSLAALMSISLFSATASAASSTDYQWTDGGIVNAVNGGGNNYVNNWSN 60
 Db 1 MFKFKNFKLFLGSLAALMSISLFSATASAASSTDYQWTDGGIVNAVNGGGNNYVNNWSN 60
 Qy 61 TGNFVKGKMTGSFRTINYNAQGWAPNGNYLTYGWRSPLEYYVWDWSWGTYRPTG 120
 Db 61 TGNFVKGKMTGSFRTINYNAQGWAPNGNYLTYGWRSPLEYYVWDWSWGTYRPTG 120
 Query Match 100 0%; Score 1171; DB 1; Length 213;
 Best Local Similarity 100 0%; Pred. No. 2.4e-80;
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MFKFKNFKLFLGSLAALMSISLFSATASAASSTDYQWTDGGIVNAVNGGGNNYVNNWSN 60
 Db 1 MFKFKNFKLFLGSLAALMSISLFSATASAASSTDYQWTDGGIVNAVNGGGNNYVNNWSN 60
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 Best Local Similarity 100 0%; Pred. No. 2.4e-80;
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 1 MFKFKNFKLFLGSLAALMSISLFSATASAASSTDYQWTDGGIVNAVNGGGNNYVNNWSN 60
 RESULT 3
 S48126 endo-1,4-beta-xylanase (BC 3.2.1.8) S precursor - *Bacillus* sp. (strain YA-14)
 N; Alternate names: xylanase S
 C; Species: *Bacillus* sp.
 A; Variety: strain YA-14
 C; Date: 14-Jul-1995 #sequence revision 22-Nov-1996 #text_change 09-Jul-2004
 C; Accession: S48126
 C; Reference number: S01734
 R; Ju-Hyun, Y.; Park, Y.S.; Yum, D.Y.; Kim, J.M.; Kong, I.S.; Bai, D.H.
 J; Microbiol. Biotechnol. 3, 139-145, 1993
 A; Title: Nucleotide sequence and analysis of a xylanase gene (xynS) from alkali-tolerant
 A; Reference number: S48126
 A; Accession: S48126
 A; Molecule type: DNA
 A; Cross-references: UNIPROT:059256; UNIPARC:UPI0000060D47; EMBL:X59058; NID:9458800; PID:9458800; PID:UNIPARC:UPI0000060D47; EMBL:X59058; NID:9458800; PID
 A; Experimental source: strain YA-14
 C; Genetics:
 A; Gene: xynS
 C; Function: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
 A; Pathway: xylan degradation
 C; Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C; Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
 F; 1-28/Domain: signal sequence #status predicted <SIG>
 F; 29-213/Domain: endo-1,4-beta-xylanase S #status predicted <MAT>
 F; 31-213/Domain: endo-1,4-beta-xylanase homology <XYL>
 F; 106/200/Active site: Glu #status predicted
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 Best Local Similarity 99 1%; Pred. No. 6.6e-80;
 Matches 211; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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 Db 1 MFKFKNFKLFLGSLAALMSISLFSATASAASSTDYQWTDGGIVNAVNGGGNNYVNNWSN 60
 Query Match 99 5%; Score 1165; DB 1; Length 213;
 Best Local Similarity 99 1%; Pred. No. 6.6e-80;
 Matches 211; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 61 TGNFVKGKMTGSFRTINYNAQGWAPNGNYLTYGWRSPLEYYVWDWSWGTYRPTG 120
 Db 61 TGNFVKGKMTGSFRTINYNAQGWAPNGNYLTYGWRSPLEYYVWDWSWGTYRPTG 120

Copyright (c) 1993 - 2006 Biocceleration Ltd.	GenCore version 5.1.7	30	405	34.6	229	2	S39155
OM protein - protein search, using sw model	487.956 Million cell updates/sec	31	388	33.1	954	1	S20907
Run on: February 3, 2006, 09:08:23 ; Search time 42 Seconds (without alignments)	487.956 Million cell updates/sec	32	382.5	32.7	211	1	JC1198
Title: US-10-626-724-5	1171	33	381	32.5	211	1	S48229
Perfect score: 1	MFKPKKFLVGLSALMSI.....YQVMATEGYQSSGSSNVTWV 213	34	377	32.2	789	2	S58235
Sequence: Scoring table: BLOSUM62	Gapop 10.0 , Gapext 0.5	35	375	32.0	211	2	S49542
Searched: 283416 seqs, 96216763 residues	Total number of hits satisfying chosen parameters: 283416	36	361	30.8	209	2	JC4909
		37	349.5	29.8	781	2	S51592
		38	336.5	28.7	802	2	A36910
		39	271.5	23.2	607	2	S24754
		40	264.5	22.6	607	2	S49528
		41	262	22.4	608	2	B53295
		42	245	20.9	266	1	S48865
		43	133	11.4	313	1	T04776
		44	126	10.8	50	2	A61149
		45	120	10.2	666	2	A42296
ALIGNMENTS							
RESULT 1							
I40569 endo-1,4-beta-xylanase (BC 3.2.1.8) A Precursor - Bacillus subtilis							
Nr:Alternate names: xylanase A							
C:Species: Bacillus subtilis							
C:Date: 12-Aug-1996 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004							
C:Accession: I40569; S39157; S39158; A53635; F69735; S51711.							
R:Wolf, M.; Geczi, A.; Simon, O.; Borrius, R.							
Microbiology 141, 281-290, 1995							
A:Title: Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus subtilis:							
A:Reference number: I40370; PMID:95219081; PMID:7704256							
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME							
A:Molecule type: DNA							
A:Residues: 1-22, P', 24-213 <WOL>							
A:Cross-references: UNIPARC:UPI000018429; UNIPARC:UPI000008630D; EMBL:Z34519; NID:G2995396; P1							
A:Experimental source: strain 168							
R:Palce, M.G.; Bourbonnais, R.; Desrochers, M.; Jurassak, L.; Yeguchi, M.							
Arch. Microbiol. 144, 201-206, 1986							
A:Title: A xylanase gene from Bacillus subtilis: nucleotide sequence and comparison with							
A:Reference number: S39157							
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME							
A:Molecule type: DNA							
A:Residues: 1-213 <PA11>							
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A:Experimental source: strain PAP15							
A:Accession: S39158							
A:Molecule type: Protein							
A:Residues: 29-58-70-73-75-76 <PA12>							
A:Cross-references: UNIPARC:UPI000015759E; UNIPARC:UPI0000172962; UNIPARC:UPI0000172963							
A:Experimental source: strain PAP15							
R:Miao, S.; Ziser, L.; Aeberold, R.; Withers, S. G.							
Biochemistry 33, 7027-7032, 1994							
A:Title: Identification of glutamic acid 78 as the active site nucleophile in Bacillus s							
A:Reference number: A53635; PMID:94271752; PMID:7911679							
A:Accession: A53635							
A:Status: Preliminary							
A:Molecule type: protein							
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A:Cross-references: UNIPARC:UPI0000172964							
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Carter, N.M.; Cho, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Ferranti, E.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Galler, J.; Harwood, C.R.; Henau, A.; Holsapple, S.; Kurama, K.; Lapidus, A.; Mardino, Koetter, P.; Koningsstein, G.; Krugh, S.; Kumano, M.; Levine, A.; Liu, H.; Masuda, S.; Mauel, Y.; Miao, C.; Ogiwara, K.; Oudega, B.; Park, S.H.; Parr, V.; Pohl, T.M.; Scanlon, R.; Schnoer, R.; Sekiguchi, J.; Sekowska, A.; Seror, Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Togoni, V.; Uchiyama, Y.							
Nature 390, 249-256, 1997							
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, R.; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Carter, N.M.; Cho, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Ferranti, E.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Galler, J.; Harwood, C.R.; Henau, A.; Holsapple, S.; Kurama, K.; Lapidus, A.; Mardino, Koetter, P.; Koningsstein, G.; Krugh, S.; Kumano, M.; Levine, A.; Liu, H.; Masuda, S.; Mauel, Y.; Miao, C.; Ogiwara, K.; Oudega, B.; Park, S.H.; Parr, V.; Pohl, T.M.; Scanlon, R.; Schnoer, R.; Sekiguchi, J.; Sekowska, A.; Seror, Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Togoni, V.; Uchiyama, Y.							
SUMMARIES							
Result No. Score Match Length DB ID Description							
1	1171	100.0	213	1	I40569	endo-1,4-beta-xylanase	
2	1168	99.7	213	1	S01734	endo-1,4-beta-xylanase	
3	1165	99.5	213	1	S48126	endo-1,4-beta-xylanase	
4	864.5	73.8	210	1	C83762	endo-1,4-beta-xylanase	
5	651.5	55.6	241	2	T37005	endo-1,4-beta-xylanase	
6	637	54.4	240	1	JS0591	endo-1,4-beta-xylanase	
7	621	53.0	240	1	S47512	endo-1,4-beta-xylanase	
8	609.5	52.0	644	1	I40712	endo-1,4-beta-xylanase	
9	600	51.2	225	1	S55747	endo-1,4-beta-xylanase	
10	594	50.7	333	1	JS0590	endo-1,4-beta-xylanase	
11	594	50.7	335	2	T50601	endo-1,4-beta-xylanase	
12	578	49.4	232	2	JC7577	endo-1,4-beta-xylanase	
13	577	49.3	221	1	S57469	endo-1,4-beta-xylanase	
14	552	47.1	227	2	S43919	endo-1,4-beta-xylanase	
15	540	46.1	219	2	S71472	endo-1,4-beta-xylanase	
16	530	44.3	197	1	A44597	endo-1,4-beta-xylanase	
17	525	44.8	221	2	JC7307	endo-1,4-beta-xylanase	
18	523	44.7	190	1	A44595	endo-1,4-beta-xylanase	
19	515.5	44.0	241	2	S71473	endo-1,4-beta-xylanase	
20	513	43.8	190	1	A44593	endo-1,4-beta-xylanase	
21	506	43.2	190	1	A44594	endo-1,4-beta-xylanase	
22	505	43.1	223	2	S39883	endo-1,4-beta-xylanase	
23	503	43.0	222	2	S39154	endo-1,4-beta-xylanase	
24	480	41.0	354	1	S51779	endo-1,4-beta-xylanase	
25	469	40.1	661	1	S59633	endo-1,4-beta-xylanase	
26	461.5	39.4	228	1	WWSXP	endo-1,4-beta-xylanase	
27	436	37.2	656	1	S12745	endo-1,4-beta-xylanase	
28	420	35.9	261	1	Q1935	endo-1,4-beta-xylanase	
29	409	34.9	511	1		endo-1,4-beta-xylanase	

Qy	121	TYKGTIVSKDGGTYDIYTTRYNAPSIDGDRRTFTQWMSVRQSKRPTGSNATITFSNHVNA	180	Qy	5	KRNFLVGG--LSAALMSISLFSATASAATST-----DYGQWTDGGGIVNAVNGSG	51			
Db	121	TYKGTIVSKDGGTYDIYTTRYNAPSIDGDRRTFTQWMSVRQSKRPTGSNATITFSNHVNA	180	Db	23	RRGFLGGAGTIALATASGGLLPGTAIAATTITNGTGTGDMYSSFTDGGSSVSMTLNGG	82			
Qy	181	WKSHEGMNIGSNWYQVMATEGYGSSGSNNVTW	213	Qy	52	GNSYVWSNTGNGENFVGKGMWTTGSPFRTINTNAGWAPNGNGYLTYGWTSPSPLIEYYVVD	111			
Db	181	WKSHEGMNIGSNWYQVMATEGYGSSGSNNVTW	213	Db	83	GSYSTQWMTNCNFVAGKGWSTGD--GNYRNY-GYNFNGNGCGLGWTNSNPLVEYYVVD	139			
RESULT 4										
C83762		endo-1,4-beta-xylanhydrolase BH0899 [imported] - <i>Bacillus halodurans</i> (strain C-125)		Qy	112	SWGTRPTGTYKGTVKSDGGYDIYTTRYNAPSIDGDRRTFTQWMSVRQSKRPTGSNAT	171			
C;Species: <i>Bacillus halodurans</i>		C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004		Db	141	NWGSYRPTGTYKGTVSDGGYDIYTTRYNAPSIDGDRRTFTQWMSVRQSKVTSGS-GT	198			
C;Accession: C83762		A;Title: Complete genome sequence of the alkaliophilic bacterium <i>Bacillus halodurans</i> and		Qy	172	ITPSNHVNAWKGHGNLGSNWYQVMATEGYGSSGSNNVTW	212			
R;Takami, H.; Nakasono, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai		A;Reference number: A83650; MUID:20512582; PMID:11058132		Db	199	ITGGMHEDAWARAGNMQGPRYMMATEGYGSSGSNNVTW	239			
C;Genetics:		A;Accession: C83762		RESULT 6						
A;Status: preliminary		A;Status: preliminary		Qy	140	ITPSNHVNAWKGHGNLGSNWYQVMATEGYGSSGSNNVTW	212			
A;Molecule type: DNA		A;Molecule type: DNA		Db	172	ITPSNHVNAWKGHGNLGSNWYQVMATEGYGSSGSNNVTW	212			
A;Residues: 1-210 <STO>		A;Residues: 1-210 <STO>		Qy	198	ITGGMHEDAWARAGNMQGPRYMMATEGYGSSGSNNVTW	239			
A;Cross-references: UNIPROT:Q9KBF3;		A;Cross-references: UNIPROT:Q9KBF3;		Db	RESULT 7					
A;Experimental source: strain C-125		A;Experimental source: strain C-125		Qy	141	NWGSYRPTGTYKGTVSDGGYDIYTTRYNAPSIDGDRRTFTQWMSVRQSKVTSGS-GT	198			
C;Genetics:		A;Title: Complete genome sequence of the alkaliophilic bacterium <i>Bacillus halodurans</i> and		Db	172	ITPSNHVNAWKGHGNLGSNWYQVMATEGYGSSGSNNVTW	212			
A;Gene: BH0899		A;Accession: C83762		Qy	199	ITGGMHEDAWARAGNMQGPRYMMATEGYGSSGSNNVTW	239			
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology		C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology		Db	140	ITPSNHVNAWKGHGNLGSNWYQVMATEGYGSSGSNNVTW	212			
Query Match	73.8%	Score 864.5; DB 2; Length 210;	Matches 158; Conservative 19; Mismatches 33; Indels 3; Gaps 2;	Qy	5	KRNFLVGG--LSAALMSISLFSATASAATST-----DYGQWTDGGGIVNAVNGSG	51			
Best Local Similarity	74.2%	Pred. No. 1.6e-5/		Db	23	RRGFLGGAGTIALATASGGLLPGTAIAATTITNGTGTGDMYSSFTDGGSSVSMTLNGG	82			
Db		A;Molecule type: DNA		Qy	52	GNSYVWSNTGNGENFVGKGMWTTGSPFRTINTNAGWAPNGNGYLTYGWTSPSPLIEYYVVD	111			
Qy	1	MFKFRNFLVGSALMSISLFSATASAATST-----DYGQWTDGGGIVNAVNGSGNYSNWSN	60	Db	83	GSYSTQWMTNCNFVAGKGWSTGD--GNYRNY-GYNFNGNGCGLGWTNSNPLVEYYVVD	139			
Db	1	MFKEVTVKLUVTVIAATISCLSAVAPSA--NTYQWTDGGCTVNAATNGPGSNYSWTWD	58	Qy	112	SWGTRPTGTYKGTVKSDGGYDIYTTRYNAPSIDGDRRTFTQWMSVRQSKRPTGSNAT	171			
Qy	61	TGNEVYVKGWTTGSPFRTINTNAGWAPNGNGYLTYGWTSPSPLIEYYVVDGWTGTYRPTG	120	Db	140	NWGSYRPTGTYKGTVSSDGGYDIYTTRYNAPSIDGDRRTFTQWMSVRQSKVTSGS-GT	197			
Db	59	TGNEVYVKGWTTGSPFRTINTNAGWAPNGNGYLTYGWTSPSPLIEYYVVDGWTGTYRPTG	118	RESULT 8						
Qy	121	TYKGTIVSKDGGTYDIYTTRYNAPSIDGDRRTFTQWMSVRQSKRPTGSNATITFSNHVNA	180	Qy	5	KRNFLVGG--LSAALMSISLFSATASAATST-----DYGQWTDGGGIVNAVNGSG	51			
Db	119	THRGTIVSKDGGTYDIYTTRYNAPSIDGDRRTFTQWMSVRQSKRPTGSNATITFSNHVNA	177	Db	23	RRGFLGGAGTIALATASGGLLPGTAIAATTITNGTGTGDMYSSFTDGGSSVSMTLNGG	82			
Qy	181	WKSHEGMNIGSNWYQVMATEGYGSSGSNNVTW	213	Qy	52	GNSYVWSNTGNGENFVGKGMWTTGSPFRTINTNAGWAPNGNGYLTYGWTSPSPLIEYYVVD	111			
Db	178	WRNAGNGLGSSMSYQVLTATEGYQSSGRSNNVTW	210	Db	83	GSYSTQWMTNCNFVAGKGWSTGD--GNYRNY-GYNFNGNGCGLGWTNSNPLVEYYVVD	139			
RESULT 5										
T37005		endo-1,4-beta-xylanase - <i>Streptomyces coelicolor</i>		Qy	112	SWGTRPTGTYKGTVKSDGGYDIYTTRYNAPSIDGDRRTFTQWMSVRQSKRPTGSNAT	171			
C;Species: <i>Streptomyces coelicolor</i>		C;Accession: T37005		Db	140	NWGSYRPTGTYKGTVSSDGGYDIYTTRYNAPSIDGDRRTFTQWMSVRQSKVTSGS-GT	197			
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004		R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.		Qy	172	ITPSNHVNAWKGHGNLGSNWYQVMATEGYGSSGSNNVTW	212			
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.		A;Reference number: Z21616		Db	172	ITPSNHVNAWKGHGNLGSNWYQVMATEGYGSSGSNNVTW	212			
Submitted to the EMBL Data Library, August 1999		A;Accession: T37005		Qy	198	ITGGMHEDAWARAGNMQGPRYMMATEGYGSSGSNNVTW	239			
A;Status: preliminary; translated from GB/EMBL/DDBJ		A;Molecule type: DNA		Db	RESULT 9					
C;Genetics:		A;Residues: 1-241 <OLI>		Qy	147	S47512				
Db		A;Experimental source: strain A3(2)		Qy	148	Best Local Similarity 58.4%; Pred. No. 1.3e-41; Mismatches 50; Indels 17; Gaps 6;				
Matches 129; Conservative 25; Mismatches 50; Indels 17; Gaps 6;		C;Superfamily: SCOBD-SCUJ1.34C		Db	149	Best Local Similarity 58.4%; Pred. No. 1.3e-41; Mismatches 50; Indels 17; Gaps 6;				

C;Species: Streptomyces sp.	Best Local Similarity 57.4%; Pred. No. 5.1e-38;
C;Accession: S47512	Matches 124; Conservative 29; Mismatches 44; Indels 19; Gaps 7;
R;Mary-Servais, C.; Moreau, A.; Gerard, C.; Dusart, J.	Qy 9 LVGLAA-ALMSISLSFATASAASTD-----YQWNTDGGIVNAVNGSGNNSV 56
Submitted to the EMBL Data Library, August 1994	Db 20 LTGLIAAGALVAGATAAASPAAAATTSNTGTHDGGSFSTWDTSGSVMDLNSGGT- 78
A;Description: Cloning and sequencing of a xylanase-encoding gene from Streptomyces sp.	Qy 57 NWSNTGNFNVGKGMTTGSPFRTINNAGWAPNGYLTLGWTSPRPLIYVWVSGTY 116
A;Reference number: S47512	Db 79 RWSNTGNFNVAGKGMGGGR-KTVSY-SQDNPNSRDAYLTLYGWTSPLVYYVWSGTY 136
A;Molecule type: DNA	Qy 117 RPTGTYKGTVKSDGTYDITYTTRYNAPSIDGDRTTFTQWVSRQSKRPTGSNATITFSN 176
A;Residues: 1-40 <MAZ>	Db 137 RPTGFMGTVTSDDGTYDITYTQWVSRQKRTEG--TTSGN 193
A;Cross-references: UNIPROT:Q56013; UNIPARC:UPI00000421AE; EMBL:X81045; NID:9531767; PID	Qy 177 HVNAWKSQHGNLGSNWAYQWVATEQYQSSSSNTV 212
A;Experimental source: strain EC3	Db 194 HFDWAKSGHNLGRH-NYIMIMATEQYQSSSSNTV 228
C;Function: catalyzes the hydrolysis of 1,4-beta-xylanose bonds in xyloans	RESULT 9
A;Pathway: Xylan degradation	S57477
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology	N:Alternate names: xylanase 1
A;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation	C;Species: <i>Emericella nidulans</i> , <i>Aspergillus nidulans</i>
P;1-47/Domain: signal sequence #status predicted <SIG>	C;Date: 10-Oct-1995 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
P;48-240/Product: endo-1,4-beta-xylanase #status predicted <MAT>	C;Accession: S57477
F;62-239/Domain: endo-1,4-beta-xylanase homology <XYL>	R;Perez-Gonzalez, J.A.
F;115-226/Active site: Glu #status predicted	submitted to the EMBL Data Library, June 1995
Qy 5 KNPFLG---LSAALMSISLSFATASAAST-----DYNQWNTDGGIVNAVNGSG 51	A;Description: Expression in <i>Saccharomyces cerevisiae</i> of two xylanase encoding genes frc
Db 23 RRGFLGGAGTVYALATAGLILPSTAAATTITTTQTYDGMYYSPWTGGGSVNTLNGG 82	A;Reference number: S57469
Qy 52 GNYSVWNTGNFNVGKGMTCNENAVKGWGNNGGR-RTVY-SCYVSPNGCYGWTSPVYVVD 111	A;Molecule type: DNA
Db 83 GSYSTQWTCNCNEAVKGWGNNGGR-RTVY-SCYVSPNGCYGWTSPVYVVD 140	A;Residues: 1-225 <PER>
Qy 112 SWGTYRPTGTYKGTVKSDGTYDITYTTRYNAPSIDGDRTTFTQWVSRQSKRPTGSNAT 171	A;Cross-references: UNIPROT:PS55332; UNIPARC:UPI0000139073; EMBL:249892; NID:9870832; PID
Db 141 NWGSTRPTGTYRPTGTYKGTVKSDGTYDITYTTRYNAPSIEGR-TFDQWVSRQSKT-VIGSGT 197	C;Genetics:
Qy 172 ITFSENWVNAWKSQHGNLGSNWAYQWVATEQYQSSSSNTV 212	A;Introns: 93/2
Db 198 ITTGNEHFDWAWAGHNLGSQFOYIMIMATEQYQSSSSNTV 238	C;Function:
RESULT 8	A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xyloans
I4 0712 endo-1,4-beta-xylanase (EC 3.2.1.8) D precursor - Cellulomonas fimi	A;Pathway: xylan degradation
N;Alternate names: xylanase D	C;Superfamily: endo-1,4-beta-xylanase homology
C;Species: Cellulomonas fimi	C;Keywords: Glycosidase; hydrolase; polysaccharide degradation
C;Accession: I40712	P;1-19/Domain: signal sequence #status predicted <SIG>
R;Mallard-Ward-Sadler, S.J.; Poole, D.M.; Henrissat, B.; Hazlewood, G.P.; Clarke, J.H.; Gill	F;20-225/Product: endo-1,4-beta-xylanase 1 #status predicted <MAT>
Mol. Microbiol. 11, 375-382, 1994	E;48-225/Domain: endo-1,4-beta-xylanase homology <XYL>
A;Title: Evidence for a general role for high-affinity non-catalytic cellulose binding c	F;121,212/Active site: Glu #status predicted
A;Accession: I40712	Query Match 51.2%; Score 600; DB 1; Length 225;
A;Status: preliminary; translated from GB/EMBL/DBJ	Best Local Similarity 56.8%; Pred. No. 8.4e-38;
A;Molecule type: DNA	Matches 121; Conservative 29; Mismatches 41; Indels 22; Gaps 8;
A;Residues: 1-44 <RES>	Qy 9 LVGLAA-ALMSISLSFATASAASTDWQN-----WTDGGIVNAVNGSGNNTG 62
A;Cross-references: UNIPROT:PS54865; UNIPARC:UPI0000139097; EMBL:X76729; NID:9558176; PID	Db 27 LAARESLURSRSTPSSTG-----WSNGYYSSPTDGGDVDTYNGAGSSYTWSNVNG 79
C;Function:	Qy 63 NPVVGKGMTCNENAVKGWGNNGGR-RTVY-GGSFPTGTYDITYTTRYNAPSIDGDRTTFTQWVSRQSKRPTGSNATITFSNHVNA 120
A;Description: catalyzes the hydrolysis of 1,4-beta-xylanose bonds in xyloans	Db 80 NPVGGKGMTCNENAVKGWGNNGGR-RTVY-GGSFPTGTYDITYTTRYNAPSIDGDRTTFTQWVSRQSKRPTGSNATITFSNHVNA 137
C;Superfamily: endo-1,4-beta-xylanase homology <NODB>	Qy 121 TYKGTVKSDGTYDITYTTRYNAPSIDGDRTTFTQWVSRQSKRPTGSNATITFSNHVNA 180
C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation	Db 138 QHRGTVYSDGATYDITYTTRYNAPSIEG-TATFEEWVSRQSKRPTG--TVTIANHFN 193
P;1-15/Domain: signal sequence #status predicted <SIG>	Qy 181 WKSQHGNLGSNWAYQWVATEQYQSSSSNTV 213
P;36-644/Product: endo-1,4-beta-xylanase D #status predicted	Db 194 WAALGMRGLGTH-NYQIVATEQYQSSSSNTV 225
P;54-229/Domain: endo-1,4-beta-xylanase homology <XYL>	RESULT 10
P;361-508/Domain: nodB homology <NODB>	JS0580
P;126,216/Active site: Glu #status predicted	endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Streptomyces lividans
Query Match 52.0%; Score 609.5; DB 1; Length 644;	N;Alternate names: xylanase B
	C;Species: Streptomyces lividans

C;Date: 10-Mar-1994 #sequence_revision 22-Nov-1996 #text_change 26-Feb-1999	Qy 93 YLTLYGWTRSPLIBYYVVDSWGTYRPTGTYKGTYSQDGTYDITYTTRYNAPSILGDRTT 152
C;Accession: JS0590; PS0239	Db 115 YLALYGWTNSNPLVEYIVDNGTYPRTGEYKGTYSQDGTYDITYTTRYNAPSILGDRTT-173
R;Shareck, P.; Roy, C.; Yaguchi, M.; Morosoli, R.; Kluepfel, D.	
Gene 107, 75-87, 1991	
A;Title: Sequences of three genes specifying xylanases in Streptomyces lividans.	Qy 153 FTOYNSVRQSKRTGSNATITPSNHNAWKSQHGNLGSNWAYQVMATEGYOSGSSNNVTV 212
A;Reference number: JS0589; MUID:92077439; PMID:1743521	Db 174 FDQYNSVRQAKRTGG---TTTGNHEDAWARAGMLGNFSYMMATEGYOSGSSNNVTV 230
A;Accession: JS0590	
A;Molecule type: DNA	
A;Residues: 1-333 <SHA>	
A;Cross-references: UNIPARC:UPI000017296A; GB: M64552	
A;Accession: PS0239	RESULT 12
A;Molecule type: protein	JC7577
A;Residues: 41-71 <SH2>	endo-1,4-beta-xylanase (EC 3.2.1.8) G2 - Aspergillus oryzae
A;Cross-references: UNIPARC:UPI000017296B	N;Alternative names: endo-1,3-beta-xylanase G2; xylanase G2
C;Genetics:	C;Species: Aspergillus oryzae
A;Gene: xlnB	C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
A;Function:	R;Kimura, T.; Suzuki, H.; Furuhashi, H.; Aburutani, T.; Morimoto, K.; Karita, S.; Sakka, Biosci. Biotechnol. Biochem. 64, 2734-2738, 2000
A;Description: catalyzes the hydrolysis of 1,4-beta-xylanase	A;Title: Molecular cloning, overexpression, and purification of a major xylanase from Aspergillus oryzae
A;Pathway: xylan degradation	A;Reference number: JC7577; PMID:11210150
A;Superfamily: Clostridium endo-1,4-beta-xylanase homology	A;Accession: JC7577
A;Keywords: extracellular protein; glycosidase; hydrolase; polyaccharide degradat	A;Molecule type: DNA
F;1-10/Domain: signal sequence #status predicted <SIG>	A;Cross-references: UNIPROT:Q9HEA4; UNIPARC:UPI0000069976; DDBJ: AB044941
F;41-333/Domain: endo-1,4-beta-xylanase B #status experimental <MAT>	A;Experimentation source: strain KBN616
F;54-230/Domain: endo-1,4-beta-xylanase homology <XYL>	A;Accession: PC7120
F;127,217/Active site: Glu #status predicted	A;Molecule type: protein
Query Match 50.7%; Score 594; DB 1; Length 333;	A;Residues: 1-232 <KIM>
Best Local Similarity 62.2%; Pred. No. 3.6e-37;	A;Cross-references: UNIPARC:UPI0000175A84
Matches 112; Conservative 19; Mismatches 43; Indels 6; Gaps 4;	C;Comment: This enzyme has strong similarity to other fungal family 11 endoxylanases, de
Qy 33 YWQNTDGGIVNAVNGSGGNYSVWSNTGNFVVGWTGSPFRTINTNAGWAWPNGNG 92	A;Genetics:
Db 56 YSFWDTSQGTTSVNMNGGGYOSTSWSRNTGNFVAGKWWANGGR-RTVQY-SGSFNPSGNA 113	A;Gene: xynG2
Db 93 YLTLYGWTRSPLIBYYVVDSWGTYRPTGTYKGTYSQDGTYDITYTTRYNAPSILGDRTT 152	A;Introns: 100/2
Db 114 YLALYGWTNSNPLVEYIVDNGTYPRTGEYKGTYSQDGTYDITYTTRYNAPSILGDRTT-172	C;Keywords: glycosidase; hydrolase
Qy 153 FTOYNSVRQSKRTGSNATITPSNHNAWKSQHGNLGSNWAYQVMATEGYOSGSSNNVTV 212	Query Match 49.4%; Score 578; DB 2; Length 232;
Db 174 FDQYNSVRQAKRTGG---TTTGNHEDAWARAGMLGNFSYMMATEGYOSGSSNNVTV 229	Best Local Similarity 52.1%; Pred. No. 3.8e-36;
RESUIT 11	Matches 122; Conservative 31; Mismatches 47; Indels 34; Gaps 9;
T50601	Qy 7 NFLVQLSAALMSIS-----LFSATA-----SAASSTD-----YWQWTDGG 41
endo-1,4-beta-xylanase (EC 3.2.1.8) B, secreted [imported] - Streptomyces coelicolor	Db 6 SILLCSAATGALAPIEPLADHPMBAFNATFNDLVGRSTPSSTGYNNGYYSSWTDDG 65
N;Alternative names: xylanase B	Qy 42 GIVNAVNGSGGNYSVWSNTGNFVVGWTGSPFRTINTNAGWAWPNGNGYLTYGWTR 101
C;Species: Streptomyces coelicolor	Db 66 GDVTYTNQNGGSYSVWSNTGNFVVGWTGSPFRTINTNAGWAWPNGNGYLTYGWTR 123
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004	Qy 102 SPLTVEYYVVDSWGTYRPTGTYKGTYSQDGTYDITYTTRYNAPSILGDRTTFTQWYSV 159
C;Accession: T50601	Db 124 DPLIKEYIVYESGYTNPGSGSGTYKQVTSRTRNASSIIIG-TATFQFWSV 182
R;Redenbach, M.; Kieser, H.M.; Denapaitis, D.; Eichner, A.; Culum, J.; Kinashi, H.; Hopw Mol. Microbiol. 21, 77-96, 1996	Qy 160 ROSKRPTGSNATITPSNHNAWKSQHGNLGSNWAYQVMATEGYOSGSSNNVTV 213
A;Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb S	Db 183 RTSKRVGG---TTTGNHEDAWARAGMLGNFSYMMATEGYOSGSSNNVTV 232
A;Reference number: Z20556; MUID:97000351; PMID:8843436	
A;Accession: T50601	
A;Status: preliminary; translated from GB/EMBL/DBJ	
A;Molecule type: DNA	RESULT 13
A;Residues: 1-335 <RED>	S57469
A;Cross-references: UNIPROT:Q9RK06; UNIPARC:UPI00000DC56B; EMBL:AL133220; PIDN: CAB61738.	endo-1,4-beta-xylanase (EC 3.2.1.8) 2 precursor - Emericella nidulans
A;Experimental source: strain A3 (2)	N;Alternative names: xylanase 2
C;Genetics:	C;Species: Emericella nidulans, Aspergillus nidulans
A;Gene: xlnB	C;Date: 10-Oct-1995 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C;Superfamily: Clostridium endo-1,4-beta-xylanase homology	R;Perez-Sonzalez, J.A.
C;Keywords: Glycosidase; hydrolase	submitted to the EMBL Data Library, June 1995
Query Match 50.7%; Score 594; DB 2; Length 335;	A;Description: Expression in Saccharomyces cerevisiae of two xylanases encoding genes frc
Best Local Similarity 62.2%; Pred. No. 3.6e-37;	A;Reference number: S57469
Matches 112; Conservative 19; Mismatches 43; Indels 6; Gaps 4;	A;Accession: S57469
Qy 33 YWQNTDGGIVNAVNGSGGNYSVWSNTGNFVVGWTGSPFRTINTNAGWAWPNGNG 92	A;Molecule type: DNA
Db 57 YSFWDTSQGTTSVNMNGGGYOSTSWSRNTGNFVAGKWWANGGR-RTVQY-SGSFNPSGNA 114	A;Residues: 1-221 <PER>
	A;Cross-references: UNIPROT:F55333; UNIPARC:UPI0000139075; EMBL: Z49893; NID:9870834; PID: 249893; Genetics:

A; Introns: 89/3
 C; Function: C; Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xyloans
 A; Pathway: xyylan degradation
 C; Superfamily: endo-1,4-beta-xyylanase; endo-1,4-beta-xyylanase homology
 C; Keywords: glycosidase; hydrolase; polysaccharide degradation
 F; 1-19/Domain: signal sequence #status predicted <SIG>
 F; 19-221/Product: endo-1,4-beta-xyylanase 1 #status predicted <MAT>
 P; 44-221/Domain: endo-1,4-beta-xyylanase homology <XYL>
 P; 117,208/Active site: Glu #status predicted

Query Match 49 3%; Score 577; DB 1; Length 221;
 Best Local Similarity 50.1%; Pred. No. 4.2e-36;
 Matches 116; Conservative 38; Mismatches 41; Indels 34; Gaps 8;

Qy 9 LVGLSALMISLISLSTATASASTD-----YMONWITGGIIN 45
 Db 1 MVSFSSLILACCS-AVTAFAAPSDQSIARSLSERSTPSSGTGTCGGDT 58

Qy 46 AVNGSGCNXSYNWSNTGNFVUGKWTGSPFRTINYAGWAPNGNGYLTLYGWTSPBLI 105
 Db 59 YTNGDGSYTYTWEWTKVGNFVGKGNPGSS-QTISY-SGFFPSENGISVIGTQNPLI 116

Qy 106 EYYVVDSSWGTYRP-TGTWKGTVKSDGTYDITYTTRYNAPSIDSQDRTETQWNSVRSK 163
 Db 117 EYYVYESQDYNPQGTAQHQTLESQDGTSDYTAATRNAPSIEG-TATFTQWNSVRSK 175

Qy 164 RPTGSNATITPSNHVNAWKSHEGMNLGSNWAYQVMATEGYQSSGSNNVT 212
 Db 176 RTSGS--VTTQNHFPDAWSQLGMLTGH-NYQIVAVEGQSSGSASITV 220

RESULT 14
 S43919 endo-1,4-beta-xyylanase (EC 3.2.1.8) precursor - imperfect fungus (Humicola insolens)
 C; Species: Humicola insolens
 C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C; Accession: S43919
 R; Dalbøge, H.; Heldt-Hansen, H. P.
 Mol. Gen. Genet. 243, 255-260, 1994
 A; Title: A novel method for efficient expression cloning of fungal enzyme genes.
 A; Reference number: S43919; MUID:34247364; PMID:8190078
 A; Accession: S43919
 A; Molecule type: mRNA
 A; Residues: 1-227 <DAL>
 A; Cross-references: UNIPROT:P55334; UNIPARC:UPI00000421A4; EMBL:X76047; NID:9505266; PID
 C; Genetics: XYLL
 A; Function: xyylan degradation
 C; Pathway: endo-1,4-beta-xyylanase; endo-1,4-beta-xyylanase homology
 C; Keywords: glycosidase; hydrolase; polysaccharide degradation
 F; 1-19/Domain: signal sequence #status predicted <SIG>
 F; 20-227/Product: endo-1,4-beta-xyylanase #status predicted <MAT>
 P; 48-225/Domain: endo-1,4-beta-xyylanase homology <XYL>
 F; 112,212/Binding site: Glu #substrate (Tyr, Tyr, Arg) #status predicted

Query Match 47.1%; Score 552; DB 2; Length 227;
 Best Local Similarity 49.1%; Pred. No. 3.2e-34;
 Matches 114; Conservative 28; Mismatches 54; Indels 36; Gaps 9;

Qy 9 LVGLSALMISLISLSTATASASTD-----WQN-----WTDGCG 42
 Db 1 MVSFLKSVLAAATAVS-SAIIAAPPDFVPRDNSTALQARQTPNAEWHNGFYFYSWNSDGG 59

Qy 43 IYNAYNGSGENSYWMSNTGNFVUGKWTGSPFRTINYAGWAPNGNGYLTLYGWTWS 102
 Db 60 QVQYNTLLEGSPYQVWRNTGNFVGKGMPTG-RTINY-GGYPMQGNYLAYGWTWS 117

Qy 103 PLIETYVVSQWGTYRP-TGTWKGTVKSDGTYDITYTTRYNAPSIDGDPFTFQYWSR 160
 Db 118 PLVETYVIESQYTGNTPGSQAQYKTFYTDQYDIFVSTRYQNPSPIDGTR-TFQQYWSR 176

Search completed: February 3, 2006, 09:13:07
 Job time : 43 secs

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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:04:18 ; Search time 199 Seconds

(without alignments)
470.290 Million cell updates/sec

Title: US-10-626-724-5
Perfect score: 1171

Sequence: 1 MPKFKKFLVGLSAAALMSI.....YQWMATEGQSSGSSNTVW 213

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

1: geneseqP1980s:*

2: geneseqP1990s:*

3: geneseqP2000s:*

4: geneseqP2001s:*

5: geneseqP2002s:*

6: geneseqP2003as:*

7: geneseqP2003bs:*

8: geneseqP2004s:*

9: geneseqP2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1171	100.0	213	3	AAY93752	A bacteri	Aay93752 A bacteri
2	1171	100.0	213	7	ADG27541	Adc27541 Bacillus	Adc27541 Bacillus
3	1171	100.0	213	8	ADG55909	Ado55909 Bacillus	Ado55909 Bacillus
4	1171	100.0	213	8	ADJ34972	Xylanase	Adj34972 Xylanase
5	1168	99.7	213	3	AAB48532	Bacillus	Aab48532 Bacillus
6	1168	99.7	213	3	AAB48518	Bacillus	Aao18638 B subtili
7	1168	99.7	213	5	AAB18638	B subtili	Aao18624 Endo-1,4-
8	1168	99.7	213	5	AAB18624	B subtili	Adj35008 Xylanase
9	1168	99.7	213	8	ADJ35008	B. circul	Adi65728 B. circul
10	1168	99.7	213	8	ADJ166728	B. subtil	Adi66740 B. subtil
11	1168	99.7	213	8	ADJ166740	B. subtil	Aay93755 A bacteri
12	1161	99.1	213	3	AAY93755	A bacteri	Aay93753 A bacteri
13	1154	98.5	213	3	AAY93755	A bacteri	Aay93754 A bacteri
14	1149	98.1	213	3	AAY93754	A bacteri	Aay47200 Modified
15	1130	96.5	213	2	AAY47200	A bacteri	Aay93751 A bacteri
16	1130	96.5	213	3	AAY93751	A bacteri	Ado70164 Xylanase
17	1125	96.1	213	8	ADG70164	Xylanase	Adj35014 Xylanase
18	1104	94.3	213	8	ADJ35014	Xylanase	Adj35014 Xylanase
19	1097	93.7	213	8	ADJ35086	Xylanase	Aaw60732 Xylanase
20	1041	88.9	185	2	AAW60732	Xylanase	Aay98064 B. subtil
21	1041	88.9	185	3	AAY98064	B. subtil	Aab6943 B. subtil
22	1041	88.9	185	4	AAB6943	B. subtil	Aau07391 Bacillus
23	1041	88.9	185	4	AAB6941	Bacillus	Aae18441 Bacillus
24	1041	88.9	185	5	AAB6946	NL-xylanase	Aao18630 Modified

ALIGNMENTS

25	1041	88.9	185	7	ADC27530	Bacillus
26	1041	88.9	197	8	ADH10330	Xylanase
27	1041	88.9	353	4	AAB6945	Xylanase
28	1041	88.9	360	8	ADH10331	Xylanase
29	1038	88.6	185	2	AAW60730	Xylanase
30	1038	88.6	185	3	AAY98062	B. circul
31	1038	88.6	185	5	AAO18625	B circula
32	1038	88.6	185	5	AAB48523	Bacillus
33	1034	88.3	353	4	AAB6946	NL-xylanase
34	1033	88.2	185	2	AAW60279	Modified
35	1030	88.0	185	2	AAW60278	Modified
36	987	84.3	185	3	AAB48524	B. circul
37	987	84.3	185	5	AAO18629	Xylanase
38	987	84.3	185	5	AAB48523	Xylanase
39	987	84.3	185	5	AAO18630	Modified
40	987	84.3	185	8	ADG6732	B. circul
41	984	84.0	185	3	AAB48528	Xylanase
42	984	84.0	185	5	AAO18634	Modified
43	984	84.0	185	8	ADG6736	B. circul
44	979	83.6	185	3	AAB48526	Xylanase
45	979	83.6	185	5	AAO18632	Modified

RESULT 1

ID AAY93752 standard; protein; 213 AA.

XX AAY93752;

AC AAY93752;

XX DT 03-OCT-2000 (first entry)

XX DE A bacterial endo-beta-1,4-xylanase protein.

XX KW Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product; dough; dough preparation.

XX OS Bacillus subtilis.

XX PN WO200039289-A2.

XX PD 06-JUL-2000.

XX XX 17-DEC-1999; 99WO-IB002071.

XX PR 23-DEC-1998; 98GB-00028599.

XX PR 06-APR-1999; 99GB-00007805.

XX PR 15-APR-1999; 99GB-00008645.

XX (DANI-) DANISCO AS.

XX PA

XX PI Sibbosen O, Sorensen JF;

XX XX DR WPI: 2000-465744/40.

DR N-PSDB; ARA47154.

XX PT Mutant xylanase protein identified using xylanase inhibitor useful for preparing non-sticky dough for bakery products.

XX PS Claim 10; Page 108; 112pp; English.

CC The present sequence represents an endo-beta-1,4-xylanase. The specification also describes an endo-beta-1,4-xylanase inhibitor, which is obtained from wheat flour. The specification also describes a mutant xylanase protein. The xylanase is useful for preparing a foodstuff, preferably a bakery product or a substance (e.g. a dough) for making the bakery product. Wild type xylanase or mutant xylanase is useful for preparing a dough that is less sticky than a dough comprising a fungal xylanase. The xylanase inhibitor is useful for screening high degree resistance xylanases for dough preparation. The xylanase is also useful for preparing a non-sticky dough. A combination of xylanase and the

CC inhibitor is useful for calibrating and/or determining the quantity of
CC inhibitor in a wheat flour sample

XX Sequence 213 AA;

Query Match 100.0%; Score 1171; DB 3; Length 213;

Best Local Similarity 100.0%; Pred. No. 1.8e-91; Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKPKKNFLVGLSALMSISLFSATASAASDLYQWNTDGGIVNAVNGGGGNTSYVWSN 60

Db 1 MFKPKKNFLVGLSALMSISLFSATASAASDLYQWNTDGGIVNAVNGGGGNTSYVWSN 60

Qy 61 TGNFVFGKGNTGSPERTINYAGWAPNGYLTLYGWTSPLEYYVYDWSWGTYRPTG 120

Db 61 TGNFVFGKGNTGSPERTINYAGWAPNGYLTLYGWTSPLEYYVYDWSWGTYRPTG 120

Qy 121 TYKGTVKSDGTYDVTTRTRYNAPSIDGDRITFTQWYWSRQSKRPTGSNATITPSNHVNA 180

Db 121 TYKGTVKSDGTYDVTTRTRYNAPSIDGDRITFTQWYWSRQSKRPTGSNATITPSNHVNA 180

Qy 181 WKSHEGNLGSNWAYQMATGEGYQSSSSSNNTVW 213

Db 181 WKSHEGNLGSNWAYQMATGEGYQSSSSSNNTVW 213

RESULT 2

ADC27541 standard; protein; 213 AA.

XX AC ADC27541;

XX DT 18-DEC-2003 (first entry)

XX DE **Bacillus subtilis** wild-type xylanase enzyme.
XX KW xylanase; xylanase inhibitor; thermosensitivity; plant cell wall;
XX plant material; baking; processing cereal; starch production;
XX processing wood; wood pulp bleaching; animal feed; flour separation;
XX wetmilling; paper and pulp production; flour dough; hemicellulose;
XX arabinoxylan; food supplement; xylan; baking process; bread volume;
XX crumb structure; crumb appearance; shelf-life; enzyme.

XX **Bacillus subtilis**.

XX PN WO2003020923-A1.

XX PD 13-MAR-2003.

XX PF 30-AUG-2002; 2002WO-IB003797.

XX PR 04-SEP-2001; 2001GB-00021387.

XX (DANI-) DANISCO AS.

XX PI Sibbesen O, Sorensen JF;

XX WPI; 2003-332934/31.

XX DR N-PSDB; ADC27541.

XX PS Novel variant xylanase polypeptide having altered sensitivity to a

XX xylanase inhibitor and altered thermosensitivity as compared with a

XX parent xylanase enzyme, useful in baking, processing cereals, starch

XX production.

XX Disclosure; Fig 1; 63pp; English.

XX This invention relates to a novel variant xylanase protein or its fragment having xylanase activity. the variants have one or more amino acid modifications so that the protein or fragment has an altered sensitivity to a xylanase inhibitor and has an altered thermosensitivity as compared with a parent xylanase enzyme. The variant xylanases of the invention are useful for degrading or modifying a plant cell wall, and

CC for processing a plant material. They may be useful for baking, CC processing cereals, starch production, in processing wood, and enhancing CC the bleaching of wood pulp. They may also be useful for a variety of CC applications such as animal feed, flour separation (wetmilling) and paper CC and pulp production. In addition, they may also be useful for preparing a CC viscosity derived from the presence of hemicellulose or arabinoxylan in a CC solution or system comprising plant cell wall material, and for modifying CC food and/or feed supplement comprising xylan. Use of the variant xylanases in baking processes improves the properties of flour based CC doughs and products made from the doughs. The baked products have highly CC desirable characteristics with respect to blood volume, crumb structure CC and appearance and additionally have an extended shelf-life. The enzymes CC of the invention have reduced thermosensitivity and inhibitor CC sensitivity which allows a reduction in the amount of xylanase required CC for animal feed, starch production and baking. The present sequence is CC that of the full-length wild-type *Bacillus subtilis* xylanase which was CC used to create the variant xylanases of the invention.

Sequence 213 AA;

Query Match 100.0%; Score 1171; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.8e-91; Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKPKKNFLVGLSALMSISLFSATASAASDLYQWNTDGGIVNAVNGGGGNTSYVWSN 60
Db 1 MFKPKKNFLVGLSALMSISLFSATASAASDLYQWNTDGGIVNAVNGGGGNTSYVWSN 60
Qy 61 TGNFVFGKGNTGSPERTINYAGWAPNGYLTLYGWTSPLEYYVYDWSWGTYRPTG 120
Db 61 TGNFVFGKGNTGSPERTINYAGWAPNGYLTLYGWTSPLEYYVYDWSWGTYRPTG 120
Qy 121 TYKGTVKSDGTYDVTTRTRYNAPSIDGDRITFTQWYWSRQSKRPTGSNATITPSNHVNA 180
Db 121 TYKGTVKSDGTYDVTTRTRYNAPSIDGDRITFTQWYWSRQSKRPTGSNATITPSNHVNA 180
Qy 181 WKSHEGNLGSNWAYQMATGEGYQSSSSSNNTVW 213
Db 181 WKSHEGNLGSNWAYQMATGEGYQSSSSSNNTVW 213

RESULT 3

ADO55909

standard; protein; 213 AA.

XX ID ADO55909;

XX AC ADO55909;

XX DT 15-JUL-2004 (first entry)

XX DE **Bacillus subtilis** xynA Protein sequence SeqID4.
XX cellulase; microorganism; organic fertiliser; faeces; urine;
XX domestic animal; sawdust; pIYH7-39; bglC; xylanase; pIYH8-49; xynA;
XX pIYH8-62; xynD; pectate lyase; pIYH9-24; pIbA; pIYH9-46; pIbB;
XX fermentation; enzyme.

XX OS **Bacillus subtilis**.

XX XX

XX ID KR2003015943-A.

XX XX

XX PD 26-FEB-2003.

XX PR 18-AUG-2001; 2001KR-00049794.

XX PR 18-AUG-2001; 2001KR-00049794.

XX (KOBII-) KOREA BIO FERTILIZER CO LTD.

XX Lee YH, Yoon HJ;

XX DR WPI; 2003-455433/43.

XX N-PSDB; ADO55908.

XX Gene encoding cellulase, cellulase expressed by the same, microorganism
 PT containing the same gene, and organic fertilizer using the same
 PT microorganism.
 XX Claim 2; SEQ ID NO 4; 1pp; Korean.
 CC This invention relates to novel genes encoding cellulase, cellulase
 CC expressed by the same, a microorganism containing the same gene, and an
 CC organic fertilizer using the same microorganism, therefore the organic
 CC fertilizer can be rapidly produced from a mixture of the faeces and urine
 CC of domestic animals and sawdust. The microorganism *Bacillus subtilis*
 CC contains one cellulase encoding gene pLYH7-39 (bigC), two xylanase
 CC encoding genes pLYH8-49 (xyna) and pLYH8-62 (xynD) and two pectate lyase
 CC encoding genes pLYH9-24 (pela) and pLYH9-46 (pelB). The organic fertilizer
 CC is produced by inoculating an appropriate amount of the microorganism
 CC *Bacillus subtilis* into the mixture of the faeces and urine of domestic
 CC animals and sawdust and fermenting the mixture. The present sequence is
 CC that of a *Bacillus subtilis* protein which is related to the production of
 CC the organic fertilizer of the invention.
 XX Sequence 213 AA;

Query Match 100.0%; Score 1171; DB 7; Length 213;
 Best Local Similarity 100.0%; Pred. No. 1.8e-91;
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SQ 1 MFKFKRNFLVGLSAALMSISLFSATASAASDLYQNWTGGIVNAVNGSGGNYSVWN 60
 1 MFKEPKRNFLVGLSAALMSISLFSATASAASDLYQNWTGGIVNAVNGSGGNYSVWN 60
 Db 61 TGNFIVYKGMTGSPRTINTNAGWAPNGNGYLTYGWTSPLEYYVYDWSGTYRPTG 120
 Qy 61 TGNFIVYKGMTGSPRTINTNAGWAPNGNGYLTYGWTSPLEYYVYDWSGTYRPTG 120
 Db 61 TGNFIVYKGMTGSPRTINTNAGWAPNGNGYLTYGWTSPLEYYVYDWSGTYRPTG 120
 Db 121 TYKGTVKSDGTYDLYTTTRYNAPSIDGDRTTFTQWYSVRSQKPTGSNATITF 180
 Qy 121 TYKGTVKSDGTYDLYTTTRYNAPSIDGDRTTFTQWYSVRSQKPTGSNATITF 180
 Db 121 TYKGTVKSDGTYDLYTTTRYNAPSIDGDRTTFTQWYSVRSQKPTGSNATITF 180
 Qy 181 WKSHGMNLGSNWAYQMATCQYQSSSSNTVW 213
 Db 181 WKSHGMNLGSNWAYQMATCQYQSSSSNTVW 213
 Qy 181 WKSHGMNLGSNWAYQMATCQYQSSSSNTVW 213
 Db 181 WKSHGMNLGSNWAYQMATCQYQSSSSNTVW 213

RESULT 4
 ADJ34972 ID ADJ34972 standard; protein; 213 AA.
 XX AC ADJ34972;
 XX DT 22-APR-2004 (first entry)
 XX DE Xylanase from an environmental sample seq id 188.
 XX KW antibacterial; fungicide; thermostable xylanase activity;
 KW dough conditioning; beverage production; nutritional supplement;
 KW animal feed; lignin reduction; wood product; xylan; bacterial infection;
 KW fungal infection; coccidioides.
 XX Unidentified.
 OS PN WO2003106654-A2.
 XX PD 24-DEC-2003.
 XX PP 16-JUN-2003; 2003WO-US019153.
 XX PR 14-JUN-2002; 2002US-0389299P.
 XX PA (DIVE-) DIVERSA CORP.
 XX PI Steer B, Callen W, Healey S, Hazlewood G, Wu D, Blum D;
 PI Esteghlalian AJ;

XX WPI; 2004-099016/10.
 DR N-PSDB; ADJ34971.

XX Novel xylanase recombinant polypeptide useful for improving textile
 texture, treating paper, eliminating microorganisms.

XX PS SEQ ID NO 188; 570pp; English.
 XX Claim 60; SEQ ID NO 188; 570pp; English.
 CC The invention describes an isolated or recombinant polypeptide (I),
 CC having 50% or more identity to 190 300-1200 residue amino acid sequences
 CC (S1), given in the specification, over a region of 100 or more residues
 CC and the polypeptide; thermostable xylanase activity. (I) is useful for:
 CC dough conditioning; beverage production; as a nutritional supplement in
 CC animal feed; reducing lignin in a wood or a wood product; and for
 CC eliminating and protecting animals from a microorganism comprising xylan.
 CC The polynucleotide (II) encoding (I) is useful for amplifying nucleic
 CC acid encoding polypeptide having a xylanase activity which involves
 CC amplifying of a template nucleic acid with a primer pair capable of
 CC amplifying (II) or its subsequence. (I) is useful for treating and
 CC preventing bacterial infection and fungal infection e.g. coccidioides.
 CC This is the amino acid sequence of a xylanase protein isolated from an
 CC environmental sample.

XX Sequence 213 AA;
 SQ Query Match 100.0%; Score 1171; DB 8; Length 213;
 Best Local Similarity 100.0%; Pred. No. 1.8e-91;
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SQ Sequence 213 AA;
 XX AC AAB48532 standard; protein; 213 AA.
 XX DT 05-MAR-2001 (first entry)
 XX DE Bacillus subtilis xylanase.
 XX KW Bacterial; *Bacillus circulans*; xylanase; xylanase activity; XA;
 XX OS Bacillus subtilis.
 XX PN WO200068396-A2.
 XX PD 16-NOV-2000.
 XX PP 12-MAY-2000; 2000WO-US013172.
 XX PR 12-MAY-1999; 99US-0131714P.
 XX PA (XENC-) XENCOR INC.
 XX PI Bentzien JM;

XX DR WPI: 2000-679800/66.
 XX Non naturally occurring XA protein with enhanced thermophilicity,
 PT alkalophilicity or thermostability relative to the naturally occurring
 PT Bacillus circulans xylanase. They may be used as the
 XX active compound in a bleaching agent which is used for bleaching pulp
 XX

CC The present sequence is given in a specification relating to non
 CC naturally occurring xylanase activity (XA) proteins. The XA proteins
 CC comprise an amino acid sequence less than 97% identical to a naturally
 CC occurring Bacillus circulans xylanase. They are modified to exhibit
 CC enhanced thermophilicity, alkalophilicity or thermostability relative to
 CC the naturally occurring B. circulans xylanase. They may be used as the
 CC active compound in a bleaching agent which is used for bleaching pulp
 XX

Sequence 213 AA;

Query Match 99.7%; Score 1168; DB 3; Length 213;

Best Local Similarity 99.5%; Pred. No. 3_3e-91; Indels 0; Gaps 0;

Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKEKKNFLVGLSALMSISLFSATASAATDYNWTDGGIVNAVNGGGNYSVNNN 60

Db 1 MFKEKKNFLVGLSALMSISLFSATASAATDYNWTDGGIVNAVNGGGNYSVNNN 60

Qy 61 TGNFVVGKWTGSPRTINAGWAPNGYLTGWTSPLEIYVDSMGTYRPTG 120

Db 61 TGNFVVGKWTGSPRTINAGWAPNGYLTGWTSPLEIYVDSMGTYRPTG 120

Qy 121 TYKGTYSKSDGTYDIYTTRYNAPSIDGDRTTFQYWSVRQSKRTGSNATITFHNHYNA 180

Db 121 TYKGTYSKSDGTYDIYTTRYNAPSIDGDRTTFQYWSVRQSKRTGSNATITFHNHYNA 180

Qy 181 WKSHEGMNLGSNWAVQYMATCGYQSSGSNTVW 213

Db 181 WKSHEGMNLGSNWAVQYMATCGYQSSGSNTVW 213

Db 121 TYKGTYSKSDGTYDIYTTRYNAPSIDGDRTTFQYWSVRQSKRTGSNATITFHNHYNA 180

Db 121 TYKGTYSKSDGTYDIYTTRYNAPSIDGDRTTFQYWSVRQSKRTGSNATITFHNHYNA 180

Qy 181 WKSHEGMNLGSNWAVQYMATCGYQSSGSNTVW 213

Db 181 WKSHEGMNLGSNWAVQYMATCGYQSSGSNTVW 213

RESULT 6

AABA8518 ID AABA8518 standard; protein; 213 AA.

XX AC AABA8518;

XX DT 05-MAR-2001 (first entry)

XX DB Bacillus circulans endo-1,4-beta xylanase precursor.

XX OS Bacillus circulans.

XX PN WO200068396-A2.

XX PD 16-NOV-2000.

XX PF 12-MAY-2000; 2000WO-US013172.

XX PR 12-MAY-1999; 99US-0133714P.

XX PA (XENC-) XENCOR INC.

XX PI Bentzien JM;

XX DR WPI: 2000-679800/66.

XX PS Disclosure: Fig 16A; 121pp; English.

XX The present invention relates to a non-naturally occurring xylanase

CC activity (XA) protein comprising an amino acid sequence less than 97%

CC identical to a naturally occurring Bacillus circulans xylanase, where the

CC protein has been modified to exhibit enhanced thermophilicity,

CC alkalophilicity, or thermostability relative to naturally occurring B.

circulans xylanase, and has at least 5 amino acid substitutions. A bleaching agent comprising a modified xylanase is useful for bleaching pulp, in the biococonversion of lignocellulosic materials to fuels, for clarifying juice and wine, extracting coffee, plant oils and starch, producing food thickeners, altering texture in bakery products, e.g. improving the quality of dough, helping bread to rise and processing of wheat and corn for starch production, use as animal food additives to aid in the digestibility of feedstuffs and in the washing of super precision devices and semiconductors. The present sequence is a xylanase protein described in the exemplification of the invention

Sequence 213 AA;

Query Match 99.7%; Score 1168; DB 5; Length 213;
 Best Local Similarity 99.5%; Pred. No. 3.3e-91;
 Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPKEKCNFLVGLSAALMSISLFSATASAASDYYQWNTDGGIVNAVNGSGGNYSVNSN 60
 Db 1 MPKEKCNFLVGLSAALMSISLFSATASAASDYYQWNTDGGIVNAVNGSGGNYSVNSN 60
 Qy 61 TGNFVQKGWGTGSPRTINNAGWAPNGCYLTYGWRSPLEYVYDGGTYPRTG 120
 Db 61 TGNFVQKGWGTGSPRTINNAGWAPNGCYLTYGWRSPLEYVYDGGTYPRTG 120
 Qy 121 TYKGTVKSDGGTYDITYTTRNAPSIDGDRTTFTQWSVRQSKRPTGSNATITFSNHVN 180
 Db 121 TYKGTVKSDGGTYDITYTTRNAPSIDGDRTTFTQWSVRQSKRPTGSNATITFSNHVN 180
 Qy 181 WKSHEGNLGSNWQYQMATEGYQSSSSNTVW 213
 Db 181 WKSHEGNLGSNWQYQMATEGYQSSSSNTVW 213

RESULT 8

AA018624 standard; protein; 213 AA.
 AC AAO18624;
 DT 24-OCT-2002 (first entry)

DB Endo-1,4-beta xylanase precursor protein.

XX Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching; liquid clarification; coffee extraction; plant oil extraction; starch extraction; food thickener; animal food additive; mutant; mutein. OS Unidentified. PN WO200238746-A2.

XX PD 16-MAY-2002.
 XX PF 09-NOV-2001; 2001WO-US048018.
 XX PR 10-NOV-2000; 2000US-00710050.
 XX PA (XENC-) XENCOR INC.
 XX PI Bentzien, J., Dahiyat, B.;
 XX DR WPI; 2002-608200/65.

XX Novel xylanase activity protein, useful in bleaching process of pulp and in food and animal feed industry, has enhanced thermostability and alkaliophilicity.

XX Disclosure; Fig 1A; 121pp; English.
 XX

XX The present invention relates to a non-naturally occurring xylanase activity (XAA) protein comprising an amino acid sequence less than 97% identical to a naturally occurring *Bacillus circulans* xylanase, where the

protein has been modified to exhibit enhanced thermophilicity, or thermostability relative to naturally occurring B. circulans xylanase, and has at least 5 amino acid substitutions. A bleaching agent comprising a modified xylanase is useful for bleaching pulp, in the biococonversion of lignocellulosic materials to fuels, for clarifying juice and wine, extracting coffee, plant oils and starch, producing food thickeners, altering texture in bakery products, e.g. improving the quality of dough, helping bread to rise and processing of wheat and corn for starch production, use as animal food additives to aid in the digestibility of feedstuffs and in the washing of super precision devices and semiconductors. The present sequence is a xylanase protein described in the exemplification of the invention

Sequence 213 AA;

Query Match 99.7%; Score 1168; DB 5; Length 213;
 Best Local Similarity 99.5%; Pred. No. 3.3e-91;
 Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPKEKCNFLVGLSAALMSISLFSATASAASDYYQWNTDGGIVNAVNGSGGNYSVNSN 60
 Db 1 MPKEKCNFLVGLSAALMSISLFSATASAASDYYQWNTDGGIVNAVNGSGGNYSVNSN 60
 Qy 61 TGNFVQKGWGTGSPRTINNAGWAPNGCYLTYGWRSPLEYVYDGGTYPRTG 120
 Db 61 TGNFVQKGWGTGSPRTINNAGWAPNGCYLTYGWRSPLEYVYDGGTYPRTG 120
 Qy 121 TYKGTVKSDGGTYDITYTTRNAPSIDGDRTTFTQWSVRQSKRPTGSNATITFSNHVN 180
 Db 121 TYKGTVKSDGGTYDITYTTRNAPSIDGDRTTFTQWSVRQSKRPTGSNATITFSNHVN 180
 Qy 181 WKSHEGNLGSNWQYQMATEGYQSSSSNTVW 213
 Db 181 WKSHEGNLGSNWQYQMATEGYQSSSSNTVW 213

RESULT 9

ADJ35008
 ID ADJ35008 standard; protein; 213 AA.

AC ADJ35008;

DT 22-APR-2004 (first entry)

XX Xylanase from an environmental sample seq id 224.
 XX antibacterial; fungicide; thermostable xylanase activity; dough conditioning; beverage production; nutritional supplement; animal feed; lignin reduction; wood product; xyian; bacterial infection; fungal infection; coccidioides.
 XX Unidentified. OS Unidentified.

XX PN WO2003106654-A2.

XX PD 24-DEC-2003.

XX PR 16-JUN-2003; 2003WO-US019153.
 XX PR 14-JUN-2002; 2002US-0389299P.

XX PA (DIVE-) DIVERSA CORP.

XX Steer, B., Callen, W., Healey, S., Hazelwood, G., Wu, D., Blum, D.;
 XX PI Esteghlalian, A.;
 XX DR WPI; 2004-099016/10.
 XX N-PSDB; ADJ35007.

XX Novel xylanase recombinant polypeptide useful for improving textile texture, treating paper, eliminating microorganisms.
 XX Claim 60; SEQ ID NO 224; 570pp; English.
 PS

PA	(XENC-) XENCOR.	PR	23-DEC-1998;	98GB-00028599.
XX		PR	06-DEC-1999;	99GB-00007805.
PI	Bentzien J, Dahiyat BI;	PR	15-AFR-1999;	99GB-00008645.
DR	WPI; 2004-118575/12.	XX		
XX	New mutant xylanase (XA) protein comprising at least four amino acid substitutions as compared to <i>Bacillus circulans</i> xylanase, useful for bleaching (paper) pulp, and in the food and animal feed industries.	PA	(DANI-) DANISCO AS.	
PT		XX		
PT		PI	Sibbesen O, Sorensen JB;	
PT		XX		
XX	Disclosure; SEQ ID NO 13; 84pp; English.	DR	WPI; 2000-465744/40.	
XX	Mutant xylanase protein identified using xylanase inhibitor useful for preparing non-sticky dough for bakery products.	DR	N-PSB; AAA47157.	
PS		XX		
XX	The invention relates to a mutant xylanase activity (XA, endo-1,4-beta xylanase from <i>Bacillus circulans</i>) protein appearing as ADIG6730. Also included is a bleaching agent comprising the XA protein. The non-naturally occurring XA protein comprises at least four amino acid substitutions as compared to <i>Bacillus circulans</i> xylanase ADI66728. The amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64, 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30, 58, or 144. The non-naturally occurring xylanase activity (XA) protein is useful for bleaching pulp in the paper and related industries, but is also useful in the food and animal feed industries. The new protein is active at higher pH and temperature ranges than naturally occurring xylanases, simplifying incorporation of the xylanase treatment step into pulp processing, especially where the enzyme is added after hot alkali treatment. The present sequence is a xylanase from another species included for comparison.	PS	Claim 1; Page 111; 112pp; English.	
XX	Sequence 213 AA;	PS		
SQ	Query Match 99.7%; Score 1168; DB 8; Length 213; Best Local Similarity 99.5%; Pred. No. 3.3e-91; Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Query Match 99.1%; Score 1161; DB 3; Best Local Similarity 99.1%; Pred. No. 1.3e-90; Matches 211; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
Qy	1 MFKPKKNFLVGLSAALMSISLFSATASAASSTDYQWNTDGGIVNAVNGGGNYSVNWSN 60	Qy	1 MFKPKKNFLVGLSAALMSISLFSATASAASSTDYQWNTDGGIVNAVNGGGNYSVNWSN 60	
Db	1 MFKPKKNFLVGLSAALMSISLFSATASAASSTDYQWNTDGGIVNAVNGGGNYSVNWSN 60	Db	1 MFKPKKNFLVGLSAALMSISLFSATASAASSTDYQWNTDGGIVNAVNGGGNYSVNWSN 60	
Qy	61 TGNFVFGKGWTTGSPPRTINNAGWAPNGYLTLYGWTRSPLEYYVDSWGTYRPTG 120	Qy	61 TGNFVFGKGWTTGSPPRTINNAGWAPNGYLTLYGWTRSPLEYYVDSWGTYRPTG 120	
Db	61 TGNFVFGKGWTTGSPPRTINNAGWAPNGYLTLYGWTRSPLEYYVDSWGTYRPTG 120	Db	61 TGNFVFGKGWTTGSPPRTINNAGWAPNGYLTLYGWTRSPLEYYVDSWGTYRPTG 120	
Qy	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTTFTQWSVRSQKPTGSNATITFVNHNVA 180	Qy	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTTFTQWSVRSQKPTGSNATITFVNHNVA 180	
Db	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTTFTQWSVRSQKPTGSNATITFVNHNVA 180	Db	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTTFTQWSVRSQKPTGSNATITFVNHNVA 180	
Qy	181 WKSHEGNLGSNWAYQWYQMATEGYQSSGSNTVW 213	Qy	181 WKSHEGNLGSNWAYQWYQMATEGYQSSGSNTVW 213	
Db	181 WKSHEGNLGSNWAYQWYQMATEGYQSSGSNTVW 213	Db	181 WKSHEGNLGSNWAYQWYQMATEGYQSSGSNTVW 213	
RESULT 12		RESULT 13		
AY93755	ID AAY93755 standard; protein; 213 AA.	AY93753		
XX	ID AAY93753 standard; protein; 213 AA.	ID AAY93753		
AC	AY93755;	XX		
XX	DT 03-OCT-2000 (first entry)	AC AAY93753;		
DT		XX		
XX	A bacterial endo-beta-1,4-xylanase mutant XM3.	DT 03-OCT-2000 (first entry)		
DE	Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product; dough; dough preparation.	XX		
KW	Synthetic.	DE A bacterial endo-beta-1,4-xylanase mutant XM3.		
KW	OS <i>Bacillus subtilis</i> .	XX Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product; dough; dough preparation.		
OS		XX Synthetic.		
OS		OS <i>Bacillus subtilis</i> .		
PN	WO200039289-A2.	XX		
XX	PD 06-JUL-2000.	FH Key		
PD	XX /note= "wild type Ile changed to Thr"	FT Misc-difference 43		
PP	PP 17-DEC-1999; 99WO-1B002071.	FT Misc-difference 197		
XX	PP /note= "wild type Met changed to Leu"	FT Misc-difference 43		

PT	Misc-difference 203	XX	XX	OS
PT	/note= "wild type Gln changed to Lys"	XX	OS	Synthetic.
XX	XX	OS	Bacillus subtilis.	
PN	WO20039289-A2.	XX	XX	
PD	06-JUL-2000.	PN	WO20039289-A2.	
XX	XX	XX	XX	
PF	17-DEC-1999;	99WO-IB002071.	PD	06-JUL-2000.
XX	XX	XX	XX	
PR	23-DEC-1998;	98GB-0002859.	PF	17-DEC-1999;
PR	06-APR-1999;	99GB-00007805.	XX	99WO-IB002071.
PR	15-APR-1999;	99GB-00008645.	XX	
XX	XX	XX	XX	
PA	(DANI-) DANISCO AS.	PA	PA	
XX	XX	PA	PA	
PI	Sibbesen O, Sorensen JF;	XX	PI	
XX	XX	XX	PI	
DR	WPI: 2000-465744/40.	XX	XX	
DR	N-PSDB; AAA47156.	DR	WPI: 2000-465744/40.	
XX	XX	DR	AAA47156.	
PT	PT	XX	XX	
PT	Mutant xylanase protein identified using xylanase inhibitor useful for preparing non-sticky dough for bakery products.	PT	PT	
XX	XX	XX	XX	
PS	PS	XX	XX	
XX	XX	XX	XX	
PS	Claim 1; Page 109; 112pp; English.	PS	Claim 1; Page 110; 112pp; English.	
XX	XX	PS	PS	
CC	The present sequence represents a mutant endo-beta-1,4-xylanase. The specification also describes an endo-beta-1,4-xylanase inhibitor, which is obtained from wheat flour. The specification also describes a mutant xylanase protein. The xylanase is useful for preparing a foodstuff, preferably a bakery product or a substance (e.g. a dough) for making the bakery product. Wild type xylanase or mutant xylanase is useful for preparing a dough that is less sticky than a dough comprising a fungal xylanase. The xylanase inhibitor is useful for screening high degree resistance xylanases for dough preparation. The xylanase is also useful for preparing a non-sticky dough. A combination of xylanase and the inhibitor is useful for calibrating and/or determining the quantity of inhibitor in a wheat flour sample.	CC	The present sequence represents a mutant endo-beta-1,4-xylanase. The specification also describes an endo-beta-1,4-xylanase inhibitor, which is obtained from wheat flour. The specification also describes a mutant xylanase protein. The xylanase is useful for preparing a foodstuff, preferably a bakery product or a substance (e.g. a dough) for making the bakery product. Wild type xylanase or mutant xylanase is useful for preparing a dough that is less sticky than a dough comprising a fungal xylanase. The xylanase inhibitor is useful for screening high degree resistance xylanases for dough preparation. The xylanase is also useful for preparing a non-sticky dough. A combination of xylanase and the inhibitor is useful for calibrating and/or determining the quantity of inhibitor in a wheat flour sample.	
SQ	Sequence 213 AA;	SQ	Sequence 213 AA;	
Query	98.5%; Score 1154; DB 3; Length 213;	Query	98.1%; Score 1149; DB 3; Length 213;	
Best Local Similarity	98.1%; Pred. No. 5.1e-90;	Best Local Similarity	97.7%; Pred. No. 1.3e-89;	
Matches	209; Conservative 2; Mismatches 2; Indels 0; Gaps 0;	Matches	208; Conservative 2; Mismatches 3; Indels 0; Gaps 0;	
Qy	1 MFKPKKNEVNLISALMSISLFSATASAASSTDYQWNTDGGIVYNAVNQSGGGNYSVNNSN 60	Qy	1 MFKPKKNEVNLISALMSISLFSATASAASSTDYQWNTDGGIVYNAVNQSGGGNYSVNNSN 60	
Db	1 MFKPKKNEVNLISALMSISLFSATASAASSTDYQWNTDGGIVYNAVNQSGGGNYSVNNSN 60	Db	1 MFKPKKNEVNLISALMSISLFSATASAASSTDYQWNTDGGIVYNAVNQSGGGNYSVNNSN 60	
Qy	61 TGNFVYKGWTTGSPPRTINNAGWAPNGNGYLTYGWRSPLEIYTDSKGTYRPTG 120	Qy	61 TGNFVYKGWTTGSPPRTINNAGWAPNGNGYLTYGWRSPLEIYTDSKGTYRPTG 120	
Db	61 TGNFVYKGWTTGSPPRTINNAGWAPNGNGYLTYGWRSPLEIYTDSKGTYRPTG 120	Db	61 TGNFVYKGWTTGSPPRTINNAGWAPNGNGYLTYGWRSPLEIYTDSKGTYRPTG 120	
Qy	121 TYKGTVKSDGTYDITTYTTRYNAPSIDGDRTTFTQWYSRQSKRTGSNATITFSNHVNA 180	Qy	121 TYKGTVKSDGTYDITTYTTRYNAPSIDGDRTTFTQWYSRQSKRTGSNATITFSNHVNA 180	
Db	121 TYKGTVKSDGTYDITTYTTRYNAPSIDGDRTTFTQWYSRQSKRTGSNATITFSNHVNA 180	Db	121 TYKGTVKSDGTYDITTYTTRYNAPSIDGDRTTFTQWYSRQSKRTGSNATITFSNHVNA 180	
Qy	181 WKSHEGMNLGSNWAYQVLMATEGYQSSGSSNTVW 213	Qy	181 WKSHEGMNLGSNWAYQVLMATEGYQSSGSSNTVW 213	
Db	181 WKSHEGMNLGSNWAYQVLMATEGYQSSGSSNTVW 213	Db	181 WKSHEGMNLGSNWAYQVLMATEGYQSSGSSNTVW 213	
RESULT 14		RESULT 15		
ID	AY93754	ID	AAR47200	
XX	standard; protein; 213 AA.	XX	AAR47200 standard; protein; 213 AA.	
AC	AY93754;	AC	AAR47200;	
XX	XX	XX	XX	
DT	03-OCT-2000 (first entry)	DT	25-MAR-2003 (revised)	
XX	A bacterial endo-beta-1,4-xylanase mutant XN2.	XX	10-AUG-1994 (first entry)	
KW	Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product; dough; dough preparation.	KW	Modified xylanase of <i>Bacillus subtilis</i> .	

KW Xylanase; *Bacillus subtilis*; baking; bread; yeast; food; foodstuffs;
KW bread; pastry.

XX *Bacillus subtilis*.

XX Key Location/Qualifiers
Key 1; 28
Peptide /label= Signal peptide.
Misc-difference 7
FT Misc-difference 13 /note= "Wild type amino acid substituted for Lys."
FT Misc-difference 16 /note= "Wild type amino acid substituted for Thr."
FT Misc-difference 21 /note= "Wild type amino acid substituted for Phe."
FT Peptide 29 .185 /note= "Wild type amino acid substituted for Met."
FT Misc-difference 30 /label= Mature protein.
FT Misc-difference 43 /note= "Wild type amino acid substituted for Gly."
FT Misc-difference 150 /note= "Wild type amino acid substituted for Thr."
FT Misc-difference 171 /note= "Wild type amino acid substituted for Asn."
FT Misc-difference 197 /note= "Wild type amino acid substituted for Ala."
FT Misc-difference 203 /note= "Wild type amino acid substituted for Leu."
FT Misc-difference 204 /note= "Wild type amino acid substituted for Lys."
PN DE4226528-A1.
XX PD 17-FBB-1994.
XX PP 11-AUG-1992; 92DE-04226528.
XX PR 11-AUG-1992; 92DE-04226528.
XX PA (ROHMGMBH)
PI Gottschalk M, Sproessler B, Schuster E;
WPI: 1994-058089/08.
DR N-PSDB; AAQ56052.
XX PT New xylanase obtnd. from *Bacillus subtilis* - useful in baking agents for
PT increased vol. of baking prods.
XX PS Claim 4; Page 10; 11pp; German.
XX CC The modified xylanase is used as a baking agent, preferably for yeast
CC pastry and white bread. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 213 AA;

Query Match 96.5%; Score 1130; DB 2; length 213;

Best Local Similarity 95.3%; Pred. No. 5.6e-88;
Matches 203; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MFKFKENFLVGLSAALMSISLFSATASAASDLYQWNTDGGGIYNAVNGSGCGNYSVNSWN 60
Db 1 MFKPCKKFLVGLTAAMFISMATASAGTDYQWNTDGGGTNAVNGSGCGNYSVNSWN 60

Qy 61 TGNFVYKGWTTGSPRTINTYAGNWAPNGCYLTLYGWTSPLEYYVVDSWGTYRPTG 120
Db 61 TGNFVYKGWTTGSPRTINTYAGNWAPNGCYLTLYGWTSPLEYYVVDSWGTYRPTG 120

Qy 121 TYKGTVKSDGTYDIYTTRNAPSIDGDRPTFQWVSVRSKRPGSNATITFSNHVNA 180
Db 121 TYKGTVKSDGTYDIYTTRNAPSIDGDNFTFTQWVSVRSKRPGSNAAITFSNHVNA 180

Qy 181 WKSHEGNLGSNWAYQVATEGKSSCSNNTVW 213

KW xylanase; *Bacillus subtilis*; baking; bread; yeast; food; foodstuffs;
KW bread; pastry.

XX *Bacillus subtilis*.

XX Key Location/Qualifiers
Key 1; 28
Peptide /label= Signal peptide.
Misc-difference 7
FT Misc-difference 13 /note= "Wild type amino acid substituted for Lys."
FT Misc-difference 16 /note= "Wild type amino acid substituted for Thr."
FT Misc-difference 21 /note= "Wild type amino acid substituted for Phe."
FT Peptide 29 .185 /note= "Wild type amino acid substituted for Met."
FT Misc-difference 30 /label= Mature protein.
FT Misc-difference 43 /note= "Wild type amino acid substituted for Gly."
FT Misc-difference 150 /note= "Wild type amino acid substituted for Thr."
FT Misc-difference 171 /note= "Wild type amino acid substituted for Asn."
FT Misc-difference 197 /note= "Wild type amino acid substituted for Ala."
FT Misc-difference 203 /note= "Wild type amino acid substituted for Leu."
FT Misc-difference 204 /note= "Wild type amino acid substituted for Lys."
PN DE4226528-A1.
XX PD 17-FBB-1994.
XX PP 11-AUG-1992; 92DE-04226528.
XX PR 11-AUG-1992; 92DE-04226528.
XX PA (ROHMGMBH)
PI Gottschalk M, Sproessler B, Schuster E;
WPI: 1994-058089/08.
DR N-PSDB; AAQ56052.
XX PT New xylanase obtnd. from *Bacillus subtilis* - useful in baking agents for
PT increased vol. of baking prods.
XX PS Claim 4; Page 10; 11pp; German.
XX CC The modified xylanase is used as a baking agent, preferably for yeast
CC pastry and white bread. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 213 AA;

Query Match 96.5%; Score 1130; DB 2; length 213;

Best Local Similarity 95.3%; Pred. No. 5.6e-88;
Matches 203; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MFKFKENFLVGLSAALMSISLFSATASAASDLYQWNTDGGGIYNAVNGSGCGNYSVNSWN 60
Db 1 MFKPCKKFLVGLTAAMFISMATASAGTDYQWNTDGGGTNAVNGSGCGNYSVNSWN 60

Qy 61 TGNFVYKGWTTGSPRTINTYAGNWAPNGCYLTLYGWTSPLEYYVVDSWGTYRPTG 120
Db 61 TGNFVYKGWTTGSPRTINTYAGNWAPNGCYLTLYGWTSPLEYYVVDSWGTYRPTG 120

Qy 121 TYKGTVKSDGTYDIYTTRNAPSIDGDRPTFQWVSVRSKRPGSNATITFSNHVNA 180
Db 121 TYKGTVKSDGTYDIYTTRNAPSIDGDNFTFTQWVSVRSKRPGSNAAITFSNHVNA 180

Qy 181 WKSHEGNLGSNWAYQVATEGKSSCSNNTVW 213

Search completed: February 3, 2006, 09:08:08
Job time : 201 secs

Db 181 WKSHEGNLGSNWAYQVATEGKSSCSNNTVW 213

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Scoring table:	BLOSUM62			
Gapop:	Gapext 10.0 , Gapext 0.5			
Searched:	2166443 seqs, 705528306 residues			
Total number of hits satisfying chosen parameters:	2166443			
Minimum DB seq length:	0			
Maximum DB seq length:	2000000000			
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries			
Database :	UniProt_05.80:*			
	1: uniprot_sprot:*			
	2: uniprot_trembl:*			
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES				
Result No.	Query	Match Length	DB ID	Description
1	11171 100.0	213	1 XYNA_BACSU	P18429 bacillus su
2	11668 99.7	213	1 XYNA_BACCI	P09850 bacillus ci
3	11666 99.6	213	2 Q59254 BACSU	Q59254 bacillus su
4	11655 99.5	213	2 Q59256 BACCI	Q59256 bacillus sp
5	11500 98.2	213	2 Q8RMN9 BACSU	Q8rmn9 bacillus su
6	11444 97.7	213	2 Q8RMN8_BACCI	Q8rmn8 bacillus ci
7	11044 96.2	213	2 Q32B36_BACSP	Q9zb36 bacillus sp
8	11044 94.3	213	2 Q84F19_9BACI	Q84F19 bacillus sp
9	10965 93.6	213	2 Q8VVC3_BACCI	Q8vv3 bacillus sp
10	94545 80.7	212	2 QF9B9_9BACI	Q6t1p3 uncultured
11	93545 79.9	214	2 Q6t1p3	P45705 bacillus st
12	93045 79.4	210	1 XYNA_BACCI	Q439993 aeromonas p
13	92945 79.3	211	2 Q43993_AERPU	Q71s35 bacillus fi
14	86445 73.8	210	2 Q8VVC3_BACCI	Q9kef3 bacillus ha
15	86445 73.8	210	2 QF9B9_9BACI	Q6w94 bacillus fi
16	86345 73.7	210	2 QF9B9_9BACI	Q9rbp8 xylinumicro
17	66345 56.7	335	2 Q9RQB8_9MIC0	Q56265 thermomonos
18	65945 56.3	338	2 Q56265_9BACI	Q5r198 thermomonos
19	65945 56.3	338	2 Q5R298_9BACI	Q9r172 streptomyce
20	65145 55.6	241	2 Q9R172_STRCO	Q9rmn9 streptomyce
21	64646 55.2	329	2 Q9RMH9_STRV	Q9rmn4 streptomyce
22	64545 55.1	335	2 Q9RMH9_STRV	Q76bvr2 streptomyce
23	63945 54.6	335	2 Q76bvr2_STRV	P26220 streptomyce
24	63745 54.4	240	1 XYNB_STRL1	Q8rmv7 nonumurea
25	63045 53.8	344	2 Q9RMV7_9ACTO	Q9ew99 streptomyce
26	62645 53.5	191	2 Q9RMV7_9ACTO	Q59962_9ACTO
27	62245 53.1	228	2 Q9RMV7_9ACTO	Q4wg11 aspergillus
28	62145 53.1	228	2 Q9RMV7_9ACTO	P55013 streptomyce
29	62145 53.0	240	2 Q936013_9ACTO	Q6935b5 microbulbif
30	61045 52.1	417	2 Q936013_9ACTO	P54865 cellulomona
31	60945 52.0	644	1 XYNB_STRL1	

Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzensegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshioka H.-P., Zumstein E., "The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*," *Nature* 390:249-256 (1997).

[4] MUTAGENESIS.
[5] ACTIVE SITE GLU-106.
[6] MEDLINE=94271752; PubMed=7911679;
[7] Miao S., Zibor L., Abberold R., Withers S.G., "Identification of glutamic acid 78 as the active site nucleophile in *Bacillus subtilis* xylanase using electrospray tandem mass spectrometry," *Biochemistry* 33:7027-7032 (1994).

-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic linkages in xyloans.

-1- PATHWAY: Xylan degradation.

-1- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G) family.

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EMBL; M36648; AAA22897.1; -; Genomic DNA.
EMBL; AP027866; AAB84458.1; -; Genomic DNA.
EMBL; Z99114; CAB13776.1; -; Genomic DNA.
PIR; I40569; I40569.
PDB; 1AKK; X-ray; A,B=..
SMR; P18429; 27-213.
Subtilist; BG10808; xyna.
InterPro; IPR01137; Glyco_hydro_11.
Protein; PF00457; Glyco_hydro_11; 1.
PRINTS; PR00911; GHYDRASE11.
PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
3D-structure; Complete proteome; Glycosidase; Hydrolase; Signal; Xylan degradation.

SEQUENCE	213 AA;	203345 MW;	20CB31238CC0564 CRC64;	
SIGNAL	1	28	Endo-1,4-beta-xylanase A.	
CHAIN	29	213	Nucleophile.	
ACT SITE	106	106	Proton donor (By similarity).	
ACT SITE	200	200	MUTAGEN	
MUTAGEN	106	106	200	E->S: Drastically reduced activity.
SEQUENCE	213 AA;	203345 MW;	20CB31238CC0564 CRC64;	

Query Match Score 1171; DB 1; Length 213;
Best Local Similarity Fred. No. 2, 3e-86;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1 MFKPKKRNFLVGLSAALMSISLFSATASAASTYDQWNNTDGGTIVNAVNGSGGTYRPTG
1 MFKPKKRNFLVGLSAALMSISLFSATASAASTYDQWNNTDGGTIVNAVNGSGGTYRPTG
61 TGNFVYGGKGTGTTGSPFRTINTYAGWAENGNGYLTLYGWTSPLEIYTYDWSGTYRPTG
61 TGNFVYGGKGTGTTGSPFRTINTYAGWAENGNGYLTLYGWTSPLEIYTYDWSGTYRPTG
121 TYKGTIVRSDDGTTD1YTTTRYAPSIDDDRTTQYWSYROSQKPTGSNATITSNHYNA
121 TYKGTIVRSDDGTTD1YTTTRYAPSIDDDRTTQYWSYROSQKPTGSNATITSNHYNA
181 WKSHGNLGSNWAQYOMATEGGYSSGNNVWN 213

Db	18.1	WKSHEGMNNGSWSAYQNMATEGQSSSSNTVW	213
RESULT 2			
XNNA_BACCI	STANDARD;	PRT;	213 AA.
ID_XNNA_BACCI			
AC_P0850;			
DT_01-MAR-1989 (Rel. 10, Created)			
DT_01-MAR-1989 (Rel. 10, Last sequence update)			
DT_10-MAY-2005 (Rel. 47, Last annotation update)			
DE_Endo-1,4-beta-xylosidase precursor (EC 3.2.1.8) (
DE_xylian xylanohydrolase).			
Name=xNNA;			
GN_Bacillus circulans.			
OS_Bacillales; Firmicutes; Bacteria; Bacillaceae;			
OX_NCBI_TaxID=1397;			
RN_RP_NUCLEOTIDE SEQUENCE.			
RX_MEDLINE:88303346; PubMed:3405767;			
RA_Yang R.C.A., Mackenzie C.R., Narang S.A.;			
RT_ "Nucleotide sequence of a <i>Bacillus circulans</i> xy			
Nucleic Acids Res. 16:7187-7187(1988).			
RN_RP_X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS), AND MUTATION			
RX_MEDLINE:94200322; PubMed:3019148;			
RA_Wakarchuk W.W., Campbell R.L., Sung W.L., Davoo			
RT_ "Mutational and crystallographic analyses of the			
RT_of the <i>Bacillus circulans</i> xylanase.";			
Protein Sci. 3:407-475(1994).			
RN_RP_STRUCTURE BY NMR			
RX_MEDLINE:96322313; PubMed:8756457; DOI=10.1021/b			
RA_McIntosh L.P., Hand G., Johnson P.E., Joshi M.D			
RA_Plesniak L.A., Ziser L., Wakarchuk W.W. Withers			
RT_ "The pKa of the General acid/base carboxyl group			
RT_cycles during catalysis: a 13C-NMR study of Bac			
RT_xylanase.";			
RL_Biochemistry 35:9958-9966(1996).			
CC_!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta			
CC_linkages in xylooligosaccharides.			
CC_!- PATHWAY: Xylan degradation.			
CC_!- SIMILARITY: Belongs to the glycosyl hydrola			
CC_family.			
CC_-----			
CC_This Swiss-Prot entry is copyright. It is produced			
CC_between the Swiss Institute of Bioinformatics			
CC_and the European Bioinformatics Institute. There a			
CC_use as long as its content is in no way modified			
CC_removed.			
CC_-----			
DR_EMBL; X07723; CAB30553.1; - ; Genomic_DNA.			
DR_PTR; S01734; S01734.			
DR_PDB; 1BCX; X-ray; @=29-213.			
DR_PDB; 1BVV; X-ray; @=29-213.			
DR_PDB; 1C5H; X-ray; A=29-213.			
DR_PDB; 1C5I; X-ray; A=29-213.			
DR_PDB; 1HV0; X-ray; A=29-213.			
DR_PDB; 1HV1; X-ray; A=29-213.			
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DR_PDB; 2BVY; X-ray; A=29-213.			
DR_InterPro; IPR010137; Glyco_hydro_11.			
DR_Pfam; PF00457; Glyco_hydro_11.			
DR_PRINTS; PR00911; GLYHYDRLASPL.			
DR_PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.			
DR_PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.			
DR_3D-structure; Glycosidase; Hydrolase; Signal; x			
FT_SIGNAL 1 28			
FT_CHAIN 29 213			Endo-1,4-beta-xyla
ACT SITE 106 106 Nucleophile.			
ACT-SITE 200 200 Proton donor.			
STRAND 33 38			

FT	STRAND	43	48	RC	STRAIN=168 trpc2;
FT	TURN	51	52	RA	Borrisse R.; Wolf M.;
FT	STRAND	53	59	RL	Submitted (JUL-1997) to the EMBL/GenBank/DBBJ databases.
FT	STRAND	63	70	DR	EMBL: Z34519; CAA84276.1; -; Genomic_DNA.
FT	TURN	75	76	DR	HSSP: P09850; 1XNB.
FT	STRAND	78	89	DR	SMR; Q59254; 27-213.
FT	STRAND	92	101	DR	GO; GO:0031176; F:endo-1,4-beta-xylanase activity; IEA.
FT	TURN	102	104	DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.
FT	STRAND	105	113	DR	GO; GO:0045493; P:xylan catabolism; IEA.
FT	STRAND	121	128	DR	InterPro: IPR001137; Glyco_hydro_11.
FT	TURN	129	130	DR	Pfam: PF00457; Glyco_hydro_11.
FT	STRAND	131	144	DR	PRINTS: PRO0911; GLYHYDRASE11.
FT	TURN	146	147	DR	PROSITE: PS00776; GLYCOSTYL_HYDROL_F11_1; 1.
FT	STRAND	150	160	DR	PROSITE: PS00777; GLYCOSTYL_HYDROL_F11_2; 1.
FT	STRAND	170	173	KW	Glycosidase; Hydrolase; Xylan degradation.
FT	HELIX	174	183	SQ	SEQUENCE 213 AA; 23355 MW; 21D76D4F8CE04B7 CRC64;
FT	TURN	184	185	SO	Query Match 99.5%; Score 1166; DB 2; Length 213;
FT	STRAND	191	202	SO	Best Local Similarity 99.5%; Pred. No. 5.e-86;
SQ	SEQUENCE	205	213 AA;	SO	Matches 212; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	Query Match 99.7%; Score 1168; DB 1; Length 213;	Qy	1 MFKFKNFLVGLSAALMSISLFSATASAASDLYQWNTDGGCIVNAVNGSGCGNSYNSWNS 60	Qy	1 MFKFKNFLVGLSAALMSISLFSATASAASDLYQWNTDGGCIVNAVNGSGCGNSYNSWNS 60
Db	Best Local Similarity 99.5%; Pred. No. 4e-86; Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Db	1 MFKFKNFLVGLSAALMSISLFSATASAASDLYQWNTDGGCIVNAVNGSGCGNSYNSWNS 60	Db	1 MFKFKNFLVGLSAALMSISLFSATASAASDLYQWNTDGGCIVNAVNGSGCGNSYNSWNS 60
Qy	61 TGNFVYKGWTTGSPPRTINTAGWVAPNGCYLTLWGTWTRSPLIBYYVDSWGTYRPTG 120	Qy	61 TGNFVYKGWTTGSPPRTINTAGWVAPNGCYLTLWGTWTRSPLIBYYVDSWGTYRPTG 120	Qy	61 TGNFVYKGWTTGSPPRTINTAGWVAPNGCYLTLWGTWTRSPLIBYYVDSWGTYRPTG 120
Db	61 TGNFVYKGWTTGSPPRTINTAGWVAPNGCYLTLWGTWTRSPLIBYYVDSWGTYRPTG 120	Db	61 TGNFVYKGWTTGSPPRTINTAGWVAPNGCYLTLWGTWTRSPLIBYYVDSWGTYRPTG 120	Db	61 TGNFVYKGWTTGSPPRTINTAGWVAPNGCYLTLWGTWTRSPLIBYYVDSWGTYRPTG 120
Qy	121 TYKGTVKS DGGTYDITTRTNPASIDGDRITFTQWSVROSKRPTGSNATITFISHVNA 180	Qy	121 TYKGTVKS DGGTYDITTRTNPASIDGDRITFTQWSVROSKRPTGSNATITFISHVNA 180	Qy	121 TYKGTVKS DGGTYDITTRTNPASIDGDRITFTQWSVROSKRPTGSNATITFISHVNA 180
Db	121 TYKGTVKS DGGTYDITTRTNPASIDGDRITFTQWSVROSKRPTGSNATITFISHVNA 180	Db	121 TYKGTVKS DGGTYDITTRTNPASIDGDRITFTQWSVROSKRPTGSNATITFISHVNA 180	Db	121 TYKGTVKS DGGTYDITTRTNPASIDGDRITFTQWSVROSKRPTGSNATITFISHVNA 180
Qy	181 WKSIGHMLGSWVAYQWATEQYQSSGSNNVTVW 213	Qy	181 WKSIGHMLGSWVAYQWATEQYQSSGSNNVTVW 213	Qy	181 WKSIGHMLGSWVAYQWATEQYQSSGSNNVTVW 213
Db	181 WKSIGHMLGSWVAYQWATEQYQSSGSNNVTVW 213	Db	181 WKSIGHMLGSWVAYQWATEQYQSSGSNNVTVW 213	Db	181 WKSIGHMLGSWVAYQWATEQYQSSGSNNVTVW 213
RESULT 3					
Q59254	BACSU	RA	Q59256 9BACI PRELIMINARY; PRT; 213 AA.	RA	Q59256 9BACI PRELIMINARY; PRT; 213 AA.
ID	Q59254_BACSU PRELIMINARY;	AC	Q59256; 01, Created)	AC	Q59256; 01, Created)
AC	01-NOV-1996 (TREMBLrel. 01, Created)	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
RT	"Cloning and nucleotide sequence of a xylanase gene (xynS) from Bacillus subtilis: characterization, mapping and construction of strains deficient in lichenase, celulase and xylanase."	DS	Endo-L, 4-beta-xylanase precursor (EC 3.2.1.8).	DS	Endo-L, 4-beta-xylanase precursor (EC 3.2.1.8).
DB	DB	GN	Name=xynS;	GN	Name=xynS;
GN	Name=xynA;	OS	Bacillus sp. YA-14.	OS	Bacillus sp. YA-14.
OS	Bacillus subtilis	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	RN	NCBI_TaxID=72411; NCBI_TaxID=1423;	RN	NCBI_TaxID=72411; NCBI_TaxID=1423;
OX	NCBI_TaxID=1423;	RN	NUCLEOTIDE SEQUENCE.	RN	NUCLEOTIDE SEQUENCE.
RN	NUCLEOTIDE SEQUENCE.	RC	STRAIN=168 trpc2;	RC	STRAIN=168 trpc2;
RC	STRAIN=168 trpc2;	RC	MEIDLINE=92140374; PubMed=310542;	RC	MEIDLINE=92140374; PubMed=310542;
RX	92140374; PubMed=310542;	RC	Niersbach M., Kreuzaler F., Geerse R.H., Postma P.W., Hirsch H.J.,	RC	Niersbach M., Kreuzaler F., Geerse R.H., Postma P.W., Hirsch H.J.,
RA	"Cloning and nucleotide sequence of the Escherichia coli K-12 ppsA gene, encoding PEP synthase."	RT	"Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus subtilis: characterization, mapping and construction of strains deficient in lichenase, celulase and xylanase."	RT	"Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus subtilis: characterization, mapping and construction of strains deficient in lichenase, celulase and xylanase."
RT	Mol. Gen. Genet. 231:332-336 (1992).	RT	Microbiology 141:281-290 (1995).	RT	Microbiology 141:281-290 (1995).
RN	[2]	RN	NUCLEOTIDE SEQUENCE.	RN	NUCLEOTIDE SEQUENCE.
RC	NUCLEOTIDE SEQUENCE.	DR	STRAIN=168 trpc2;	DR	STRAIN=168 trpc2;
RX	MEIDLINE=9519084; PubMed=7704256;	DR	MEIDLINE=9519084; PubMed=7704256;	DR	MEIDLINE=9519084; PubMed=7704256;
RA	Wolf M., Geczi A., Simon O., Borrisse R.;	DR	Wolf M., Geczi A., Simon O., Borrisse R.;	DR	Wolf M., Geczi A., Simon O., Borrisse R.;
RT	"Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus subtilis: characterization, mapping and construction of strains deficient in lichenase, celulase and xylanase."	RT	"Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus subtilis: characterization, mapping and construction of strains deficient in lichenase, celulase and xylanase."	RT	"Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus subtilis: characterization, mapping and construction of strains deficient in lichenase, celulase and xylanase."
RT	Microbiology 141:281-290 (1995).	RT	Microbiology 141:281-290 (1995).	RT	Microbiology 141:281-290 (1995).
RN	[3]	RP	NUCLEOTIDE SEQUENCE.	RP	NUCLEOTIDE SEQUENCE.
RP	NUCLEOTIDE SEQUENCE.	DR	STRAIN=168 trpc2;	DR	STRAIN=168 trpc2;
RP	NUCLEOTIDE SEQUENCE.	DR	MEIDLINE=9519084; PubMed=7704256;	DR	MEIDLINE=9519084; PubMed=7704256;
RA	Wolf M., Geczi A., Simon O., Borrisse R.;	DR	Wolf M., Geczi A., Simon O., Borrisse R.;	DR	Wolf M., Geczi A., Simon O., Borrisse R.;
RT	"Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus subtilis: characterization, mapping and construction of strains deficient in lichenase, celulase and xylanase."	RT	"Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus subtilis: characterization, mapping and construction of strains deficient in lichenase, celulase and xylanase."	RT	"Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus subtilis: characterization, mapping and construction of strains deficient in lichenase, celulase and xylanase."
RT	Microbiology 141:281-290 (1995).	RT	Microbiology 141:281-290 (1995).	RT	Microbiology 141:281-290 (1995).
RN	[3]	RP	NUCLEOTIDE SEQUENCE.	RP	NUCLEOTIDE SEQUENCE.
RP	NUCLEOTIDE SEQUENCE.	DR	STRAIN=168 trpc2;	DR	STRAIN=168 trpc2;
RP	NUCLEOTIDE SEQUENCE.	DR	MEIDLINE=9519084; PubMed=7704256;	DR	MEIDLINE=9519084; PubMed=7704256;
RA	Wolf M., Geczi A., Simon O., Borrisse R.;	DR	Wolf M., Geczi A., Simon O., Borrisse R.;	DR	Wolf M., Geczi A., Simon O., Borrisse R.;
RT	"Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus subtilis: characterization, mapping and construction of strains deficient in lichenase, celulase and xylanase."	RT	"Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus subtilis: characterization, mapping and construction of strains deficient in lichenase, celulase and xylanase."	RT	"Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus subtilis: characterization, mapping and construction of strains deficient in lichenase, celulase and xylanase."
RT	Microbiology 141:281-290 (1995).	RT	Microbiology 141:281-290 (1995).	RT	Microbiology 141:281-290 (1995).
RN	[3]	RP	NUCLEOTIDE SEQUENCE.	RP	NUCLEOTIDE SEQUENCE.

DR	PROSITE; PS00776; GLYCOSYL HYDROL_F11_1; 1.	Qy	181 WKSHEMNLLGSNWAVQVMATEGYQSSGSSNVTW 213
DR	PROSITE; PS00777; GLYCOSYL HYDROL_F11_2; 1.	Db	181 WKSHEMNLLGSNWAVQVMATEGYQSSGSSNVTW 213
KW	Glycosidase; Hydrolase; Signal; Xylan degradation.		
FT	SIGNAL 1 28		
FT	CHAIN 29 213 endo-1, 4-beta-xylanase.		
SQ	SEQUENCE 213 AA; 23341 MW; 2110D3576CC034 CRC64;		
	Query Match 99 5%; Score 1165; DB 2; Length 213;		
	Best Local Similarity 99.1%; Pred. No. 7e-86; 2; Mismatches 0; Indels 0; Gaps 0;		
	Matches 211; Conservative 2; Nucleotide sequence update)		
Qy	1 MFKFKFQFLVGLSAAALMSISLFSATASAASSTDYQWNTDGGIVNAVNGGGNYSVNWN 60	RESULT 6	
Db	1 MFKFKFQFLVGLSAAALMSISLFSATASAASSTDYQWNTDGGIVNAVNGGGNYSVNWN 60	Q8RNN8 BACCI PRELIMINARY; PRT; 213 AA.	
Qy	61 TGNFVVGKGMTTGSPRTINNAGWAPNGNGYLTLGYWTRSPLEYYVDSWGTYRPTG 120	ID Q8RNN8_BACCI PRELIMINARY; PRT; 213 AA.	
Db	61 TGNFVVGKGMTTGSPRTINNAGWAPNGNGYLTLGYWTRSPLEYYVDSWGTYRPTG 120	ID Q8RNN8_BACCI PRELIMINARY; PRT; 213 AA.	
Qy	121 TYKGTVKSDFGTYDYYTTRYNAPSIDGDRITFTQWYSVRSKRPTGSNATITFENHVN 180	RP NUCLEOTIDE SEQUENCE.	
Db	121 TYKGTVKSDFGTYDYYTTRYNAPSIDGDRITFTQWYSVRSKRPTGSNATITFENHVN 180	Sun J., Xu Z., Li W., Gu S., Zhao H., Xiao J., Chen Y.; Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.	
Qy	181 WKSHEMNLLGSNWAVQVMATEGYQSSGSSNVTW 213	RL DEO; GO:0009881; AAC08360.1; -; Genomic_DNA.	
Db	181 WKSHEMNLLGSNWAVQVMATEGYQSSGSSNVTW 213	OS Bacillus circulans.	
	Query Match 99 5%; Score 1165; DB 2; Length 213;	OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	
	Best Local Similarity 99.1%; Pred. No. 7e-86; 2; Mismatches 0; Indels 0; Gaps 0;	NCBI_TaxID:1377;	
	Matches 211; Conservative 2; Nucleotide sequence update)	DR SMR; Q8RNN8; 1XNB.	
Qy	1 MFKFKFQFLVGLSAAALMSISLFSATASAASSTDYQWNTDGGIVNAVNGGGNYSVNWN 60	RP NUCLEOTIDE SEQUENCE.	
Db	1 MFKFKFQFLVGLSAAALMSISLFSATASAASSTDYQWNTDGGIVNAVNGGGNYSVNWN 60	Sun J., Xu Z., Li W., Gu S., Zhao H., Xiao J., Chen Y.; Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.	
Qy	61 TGNFVVGKGMTTGSPRTINNAGWAPNGNGYLTLGYWTRSPLEYYVDSWGTYRPTG 120	RL DEO; GO:0009881; AAC08360.1; -; Genomic_DNA.	
Db	61 TGNFVVGKGMTTGSPRTINNAGWAPNGNGYLTLGYWTRSPLEYYVDSWGTYRPTG 120	OS Bacillus circulans.	
Qy	121 TYKGTVKSDFGTYDYYTTRYNAPSIDGDRITFTQWYSVRSKRPTGSNATITFENHVN 180	OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	
Db	121 TYKGTVKSDFGTYDYYTTRYNAPSIDGDRITFTQWYSVRSKRPTGSNATITFENHVN 180	NCBI_TaxID:1423;	
	Query Match 99 5%; Score 1165; DB 2; Length 213;	DR SMR; Q8RNN9; 1XNB.	
	Best Local Similarity 99.1%; Pred. No. 7e-86; 2; Mismatches 0; Indels 0; Gaps 0;	RP NUCLEOTIDE SEQUENCE.	
	Matches 210; Conservative 2; Nucleotide sequence update)	RA GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . . ; IEA.	
Qy	1 MFKFKFQFLVGLSAAALMSISLFSATASAASSTDYQWNTDGGIVNAVNGGGNYSVNWN 60	RA GO:0005975; P:carbohydrate metabolism; IEA.	
Db	1 MFKFKFQFLVGLSAAALMSISLFSATASAASSTDYQWNTDGGIVNAVNGGGNYSVNWN 60	DR GO:0045493; P:xylan catabolism; IEA.	
Qy	61 TGNFVVGKGMTTGSPRTINNAGWAPNGNGYLTLGYWTRSPLEYYVDSWGTYRPTG 120	DR InterPro; IPR001137; Glyco_hydro_11.	
Db	61 TGNFVVGKGMTTGSPRTINNAGWAPNGNGYLTLGYWTRSPLEYYVDSWGTYRPTG 120	DR Pfam; PF00457; Glyco_hydro_11.	
Qy	121 TYKGTVKSDFGTYDYYTTRYNAPSIDGDRITFTQWYSVRSKRPTGSNATITFENHVN 180	DR PRINTS; PS00911; GLYHYDROLASE11.	
Db	121 TYKGTVKSDFGTYDYYTTRYNAPSIDGDRITFTQWYSVRSKRPTGSNATITFENHVN 180	DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.	
	Query Match 97.7%; Score 1144; DB 2; Length 213;	DR XY1an degradation.	
	Best Local Similarity 97.7%; Pred. No. 3.4e-84; 1; Mismatches 4; Indels 0; Gaps 0;	DR SEQUENCE 213 AA; 23378 MW; E306B98D49E8CF4D CRC64;	
Qy	1 MFKFKFQFLVGLSALMSISLFSATASAASSTDYQWNTDGGIVNAVNGGGNYSVNWN 60	RESULT 7	
Db	1 MFKFKFQFLVGLSALMSISLFSATASAASSTDYQWNTDGGIVNAVNGGGNYSVNWN 60	Q9ZB36_BACSP PRELIMINARY; PRT; 213 AA.	
	Query Match 97.7%; Score 1144; DB 2; Length 213;	ID Q9ZB36_BACSP PRELIMINARY; PRT; 213 AA.	
	Best Local Similarity 97.7%; Pred. No. 3.4e-84; 1; Mismatches 4; Indels 0; Gaps 0;	AC Q9ZB36; 10, Created)	
	Matches 208; Conservative 1; Nucleotide sequence update)	DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)	
DE	Endo-1, 4-xylanase.	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
OS	Bacillus subtilis.	DR Endo-1, 4-xylanase.	
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	DR Name=xynA;	
RN	NCBI_TaxID:1423;	OS Bacillus sp.	
	Query Match 97.7%; Score 1144; DB 2; Length 213;	DR SMR; Q8RNN9; 1XNB.	
	Best Local Similarity 97.7%; Pred. No. 3.4e-84; 1; Mismatches 4; Indels 0; Gaps 0;	RP NUCLEOTIDE SEQUENCE.	
	Matches 208; Conservative 1; Nucleotide sequence update)	RA GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . . ; IEA.	
Qy	1 MFKFKFQFLVGLSAAALMSISLFSATASAASSTDYQWNTDGGIVNAVNGGGNYSVNWN 60	RA GO:0005975; P:carbohydrate metabolism; IEA.	
Db	1 MFKFKFQFLVGLSAAALMSISLFSATASAASSTDYQWNTDGGIVNAVNGGGNYSVNWN 60	DR GO:0045493; P:xylan catabolism; IEA.	
Qy	61 TGNFVVGKGMTTGSPRTINNAGWAPNGNGYLTLGYWTRSPLEYYVDSWGTYRPTG 120	DR InterPro; IPR001137; Glyco_hydro_11.	
Db	61 TGNFVVGKGMTTGSPRTINNAGWAPNGNGYLTLGYWTRSPLEYYVDSWGTYRPTG 120	DR Pfam; PF00457; Glyco_hydro_11.	
Qy	121 TYKGTVKSDFGTYDYYTTRYNAPSIDGDRITFTQWYSVRSKRPTGSNATITFENHVN 180	DR PRINTS; PS00911; GLYHYDROLASE11.	
Db	121 TYKGTVKSDFGTYDYYTTRYNAPSIDGDRITFTQWYSVRSKRPTGSNATITFENHVN 180	DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.	
	Query Match 98.2%; Score 1150; DB 2; Length 213;	DR XY1an degradation.	
	Best Local Similarity 98.6%; Pred. No. 1.1e-84; 1; Mismatches 2; Indels 0; Gaps 0;	DR SEQUENCE 213 AA; 23277 MW; 34DFAD49D2C034 CRC64;	
Qy	1 MFKFKFQFLVGLSAAALMSISLFSATASAASSTDYQWNTDGGIVNAVNGGGNYSVNWN 60	RESULT 7	
Db	1 MFKFKFQFLVGLSAAALMSISLFSATASAASSTDYQWNTDGGIVNAVNGGGNYSVNWN 60	Q9ZB36_BACSP PRELIMINARY; PRT; 213 AA.	
	Query Match 98.2%; Score 1150; DB 2; Length 213;	ID Q9ZB36_BACSP PRELIMINARY; PRT; 213 AA.	
	Best Local Similarity 98.6%; Pred. No. 1.1e-84; 1; Mismatches 2; Indels 0; Gaps 0;	AC Q9ZB36; 10, Created)	
	Matches 210; Conservative 1; Nucleotide sequence update)	DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)	
Qy	1 MFKFKFQFLVGLSAAALMSISLFSATASAASSTDYQWNTDGGIVNAVNGGGNYSVNWN 60	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
Db	1 MFKFKFQFLVGLSAAALMSISLFSATASAASSTDYQWNTDGGIVNAVNGGGNYSVNWN 60	DR Endo-1, 4-beta-xylanhydrolase.	
	Query Match 98.2%; Score 1150; DB 2; Length 213;	DR Name=xynA;	
	Best Local Similarity 98.6%; Pred. No. 1.1e-84; 1; Mismatches 2; Indels 0; Gaps 0;	OS Bacillus; Firmicutes; Bacillales; Bacillaceae; Bacillus.	
	Matches 210; Conservative 1; Nucleotide sequence update)	NCBI_TaxID:1409;	
Qy	61 TGNFVVGKGMTTGSPRTINNAGWAPNGNGYLTLGYWTRSPLEYYVDSWGTYRPTG 120	DR NUCLEOTIDE SEQUENCE.	
Db	61 TGNFVVGKGMTTGSPRTINNAGWAPNGNGYLTLGYWTRSPLEYYVDSWGTYRPTG 120	RA Kim S.C.; Jeong K.J.; Kim M.S.;	
Qy	121 TYKGTVKSDFGTYDYYTTRYNAPSIDGDRITFTQWYSVRSKRPTGSNATITFENHVN 180	DR Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.	
Db	121 TYKGTVKSDFGTYDYYTTRYNAPSIDGDRITFTQWYSVRSKRPTGSNATITFENHVN 180	DR HSSP; P03850; 1XNB.	
	Query Match 98.2%; Score 1150; DB 2; Length 213;	DR SMR; Q9ZB36; 27-213.	

DR	GO:0016787; F:hydrolase activity; IEA.	Db	1 MFKFKNFKFLVGLTAALMSISLFSANASAATDYNQNWTGGTVAVNGSGCGNYSYVNSWN 60
DR	GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.	Qy	61 TGNFVKGKMTGSFRTINNAGWAPNGNGYLTLGYWTRSPLEYYVVDWSWGTYRPTG 120
DR	GO:0005975; F:carbohydrate metabolism; IEA.	Db	61 TGNFVKGKMTGSFRTINNAGWAPNGNGYLTLGYWTRSPLEYYVVDWSWGTYRPTG 120
DR	Pfam: PF001137; Glyco_hydro_11.	Qy	61 TGNFVKGKMTGSFRTINNAGWAPNGNGYLTLGYWTRSPLEYYVVDWSWGTYRPTG 120
DR	PRINTS; PRO0911; GLYDRLAS11.	Db	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180
DR	Hydrolase; PS00776; GLYCOSYL_HYDROL_F11_1; 1.	Qy	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180
KW	Hydrolase.	Db	121 TYKGTVKSDGTYDYYTTRYDAPSIDGDKTFQWVSRQSKRPGSNATITFSNHVNA 180
SQ	SEQUENCE. 213 AA.; 23277 MW; 3A1DEE1139E3359B CRC64;	Qy	181 WKSHGMNLGSNWAYQVMTAGYQSSSSNTVW 213
Query Match	96.2%; Score 1127; DB 2; Length 213;	Qy	181 WKSHGMNLGSNWAYQVLTAGYQSSSSNTVW 213
Best Local Similarity	94.8%; Pred. No. 8e-83;	Db	181 WKSHGMNLGSNWAYQVLTAGYQSSSSNTVW 213
Matches 202; Conservative	5; Mismatches 6; Indels 0; Gaps 0;	Qy	1
1 MFKFKNFKFLVGLSAALMSISLFSATASAATDYNQNWTGGTVAVNGSGCGNYSYVNSWN 60	RESULT 9	Q8VVC3_9BACI PRELIMINARY; PRT; 213 AA.	
1 MFKFKNFKFLVGLTAAMFSISMFSAAGTDYQWQNWTGGTVAVNGSGCGNYSYVNSWN 60	Q8VVC3_9BACI PRELIMINARY; PRT; 213 AA.	Q8VVC3_9BACI PRELIMINARY; PRT; 213 AA.	
Db	61 TGNFVKGKMTGSFRTINNAGWAPNGNGYLTLGYWTRSPLEYYVVDWSWGTYRPTG 120	AC	61 TGNFVKGKMTGSFRTINNAGWAPNGNGYLTLGYWTRSPLEYYVVDWSWGTYRPTG 120
Db	61 TGNFVKGKMTGSFRTINNAGWAPNGNGYLTLGYWTRSPLEYYVVDWSWGTYRPTG 120	DT	01-MAR-2002 (TREMBLrel: 20; Created)
Db	01-OCT-2003 (TREMBLrel: 25; Last annotation update)	DT	01-MAR-2002 (TREMBLrel: 20; Last annotation update)
Qy	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180	DB	DB Endo-xylanase.
Db	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180	GN	GN Name-xyl1;
Qy	181 WKSHGMNLGSNWAYQVMTAGYQSSSSNTVW 213	OS	OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
Db	181 WKSHGMNLGSNWAYQVLTAGYQSSSSNTVW 213	OC	OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
RN	[1]	OX	OX NCBI_TaxID:165829;
RP	NUCLEOTIDE SEQUENCE.	DR	DR SMR; Q8VVC3_9BACI PRELIMINARY; PRT; 213 AA.
RA	Hong I.P., Lee S.Y., Choi S.G.;	DR	DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
RA	Submitted (OCT-2001); AAL32473.1; -; Genomic_DNA.	DR	DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
RA	EMBL; AP041773; AAL32473.1; -; Genomic_DNA.	DR	DR InterPro; IPR001137; Glyco_hydro_11.
RA	HSSP; P09850; 1XNB.	DR	DR Pfam; PF00457; Glyco_hydro_11;
RA	SMR; Q8VVC3_9BACI PRELIMINARY; PRT; 213 AA.	DR	DR PRINTS; PR00911; GLYDRASE11;
AC	Q8AF19_9BACI PRELIMINARY; PRT; 213 AA.	DR	DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1;
AC	Q8AF19_9BACI PRELIMINARY; PRT; 213 AA.	DR	DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2;
DT	01-JUN-2003 (TREMBLrel: 24; Created)	RW	RW XY1an degradation.
DT	01-OCT-2003 (TREMBLrel: 24; Last sequence update)	SQ	SQ SEQUENCE. 213 AA.; 23341 MW; 4CC0DFF525E7551 CRC64;
DB	01-OCT-2003 (TREMBLrel: 25; Last annotation update)	Qy	Query Match 93.6%; Score 1096; DB 2; Length 213;
GN	Endo-1,4-beta-xylanase A precursor.	Qy	Best Local Similarity 92.5%; Pred. No. 2.5e-80;
Bacillus sp.	Bp-7	Matches 197; Conservative 8; Mismatches 8; Indels 0; Gaps 0;	
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OC			
OX			
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.	Db	1 MFKFKNFKFLVGLTAALMSISLFSATASAATDYNQNWTGGTVAVNGSGCGNYSYVNSWN 60
RX	PubMed: DOI=10.1007/s00284-003-4196-0;	Qy	1 MFKFKNFKFLVGLTAALMSISLFSATASAATDYNQNWTGGTVAVNGSGCGNYSYVNSWN 60
RA	Gallardo O, Diaz P, Pastor F.I.J.;	Db	1 MFKFKNFKFLVGLTAALMSISLFSATASAATDYNQNWTGGTVAVNGSGCGNYSYVNSWN 60
RT	"Cloning and characterization of xylanase A from the strain Bacillus	Qy	61 TGNFVKGKMTGSFRTINNAGWAPNGNGYLTLGYWTRSPLEYYVVDWSWGTYRPTG 120
RT	sp. BP-7: comparison with alkaline pI-low molecular weight xylanases	Db	61 TGNFVKGKMTGSFRTINNAGWAPNGNGYLTLGYWTRSPLEYYVVDWSWGTYRPTG 120
RT	of family 11";	Qy	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180
RL	Curr. Microbiol. 48:276-279 (2004).	Db	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180
DR	EMBL; AY526759; CAD0654.1; -; Genomic_DNA.	Qy	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180
DR	HSSP; P09850; 1XNB.	Db	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180
DR	SMR; Q8AF19; 27-213.	Qy	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180
DR	GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.	Db	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180
DR	GO:0005975; P:carbohydrate metabolism; IEA.	Qy	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180
DR	GO:0045493; P:xyilan catabolism; IEA.	Db	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180
DR	InterPro; IPR001137; Glyco_hydro_11.	Qy	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180
DR	Pfam; PF00457; Glyco_hydro_11.	Db	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180
DR	PRINTS; PRO0911; GLYDRLAS11.	Qy	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1.	Db	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2.	Qy	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180
KW	Signal; xylan degradation.	Db	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180
PT	SIGNAL 1	Qy	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180
PT	CHAIN 213 AA.; 23475 MW; F1E194D2A329516 CRC64;	Db	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180
SQ	SEQUENC 213 AA.; 23475 MW; F1E194D2A329516 CRC64;	Qy	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180
Query Match	94.3%; Score 1104; DB 2; Length 213;	Db	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180
Best Local Similarity	93.0%; Pred. No. 5.7e-11;	Qy	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180
Matches 198; Conservative 8; Mismatches 7; Indels 0; Gaps 0;		Db	121 TYKGTVKSDGTYDYYTTRYNAPSIDGDRTFQWVSRQSKRPGSNATITFSNHVNA 180
Qy	1 MFKFKNFKFLVGLSAALMSISLFSATASAATDYNQNWTGGTVAVNGSGCGNYSYVNSWN 60	Qy	1 MFKFKNFKFLVGLSAALMSISLFSATASAATDYNQNWTGGTVAVNGSGCGNYSYVNSWN 60

DE	Xylanase A.	DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; UNKNOWN_1.
OS	Paenibacillus sp. KCTC8848P.	DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.	KW	Glycosidase; Hydrolase; Signal; Xylan degradation.	
NCBI_TaxID=10999;	FT		
[1]	SEQUENCE	SEQUAL	1
NUCLEOTIDE SEQUENCE.	SEQUENCE	29	Potential.
STRAIN=KCTC 8848P;	SEQUENCE	214 AA;	23478 MW;
RA	Query Match	79.9%; Score 935.5;	DB 2; Length 214;
Lee H.-J., Shin D.-J., Cho N.-C., Im S.-Y., Lee H.-B., Chun S.-B., Bai S.;	Best Local Similarity	80.4%; Pred. No. 2.1e-67;	
Submitted (OCV-1999) to the EMBL/GenBank/DBJ databases.	Matches	172;	Conservative 13; Mismatches 28; Indels 1; Gaps 1;
RL	Qy	1	MFKFKKFLVGLSALAIMS-TSLFLSATASAASTDWYQNTWDGGTIVNAVNGSGGNYSVNW 59
EMBL; AF195421; AAG23526.1; -; Genomic_DNA.	Db	1	MFKLSSKILMVLVLLTSMSPFLSLVYVTASTDWQNWTGGTIVNATGSDGNNSVWS 60
HSSP; P09850; 1XNB.	Qy	60	NTGNFIVNGKGWTTGSPEPTINNYAGWAWNGNGYLTLGKTRSPSLIEYYVNDNSGTYRPT 119
SMR; Q9P989; 25.2.	Db	61	NCGNPFVGKSGWTTGGATRVINYAGAFSPSGNGYIALYGTRNSLIEYYVWDNSGTYRPT 120
GO; GO:0004553; P: hydrolase activity, hydrolyzing O-glycosyl . . . ; IEA.	Qy	120	GTYKGTIVKSDGTYDLYTTRTRYNAPSIDGDRTTFTQWYSVQSKPTGSNATITFSNHVN 179
DR	Db	121	GTYKGTIVTSDGGTIDLYTTRTRYNAPSIDGDRTTFTQWYSVQSKPTGSNATITFSNHVN 180
GO; GO:000575; P: carbohydrate metabolism; IEA.	Qy	180	AWKSHGMNLGSNWAYQWVATEGYOSGSNNVTVW 213
DR	Db	181	AWKSGMNLSSWSVQVATEGYOSGSNNVTVW 214
GO; GO:004493; P: xylan catabolism; IEA.	RESULT 12		
DR	XYNA_BACT	STANDARD	PRT; 210 AA.
InterPro; IPR001137; Glyco_hydro_11.	ID	XYNA_BACT	
Pfam; PF00457; Glyco_hydro_11.	AC	P45705;	
PRINTS; PR00911; GLYDRYLASE1.	DT	01-NOV-1995 (Rel. 32, Created)	
PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; UNKNOWN_1.	DT	15-JUL-1998 (Rel. 36, Last sequence update)	
PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.	DT	10-MAY-2005 (Rel. 47, Last annotation update)	
Xylan degradation.	DE	Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (xylanase A) (1..4..	
SEQUENCE 212 AA;	DE	Endo-D-xylan xylanohydrolase A).	
Qy	1	MFKFKKFLVGLSALAIMS-TSLFLSATASAASTDWYQNTWDGGTIVNAVNGSGGNYSVNW 60	
Best Local Similarity	80.7%; Score 945.5;	DB 2; Length 212;	
Matches 169; Conservative 17; Mismatches 26; Indels 1; Gaps 1;	Db	SGNFIVNGKGWTTGSPEPTINNYAGWAWNGNGYLTLGKTRSPSLIEYYVNDNSGTYRPT 120	
RL	Qy	61	TGNFIVNGKGWTTGSPEPTINNYAGWAWNGNGYLTLGKTRSPSLIEYYVNDNSGTYRPT 120
1 MFKFKKFLVGLSALAIMS-TSLFLSATASAASTDWYQNTWDGGTIVNAVNGSGGNYSVNW 59	Db	60	SGNFIVNGKGWTTGSPEPTINNYAGWAWNGNGYLTLGKTRSPSLIEYYVNDNSGTYRPT 119
Db	Qy	121	TYKGTYKSDGTYDLYTTRTRYNAPSIDGDRTTFTQWYSVQSKPTGSNATITFSNHVN 180
1 MFKFKKFLVGLSALAIMS-TSLFLSATASAASTDWYQNTWDGGTIVNAVNGSGGNYSVNW 59	Db	120	TYKGTYKSDGTYDLYTTRTRYDAPSIDGKTTFTQWYSVQSKPTGSNATITFSNHVN 179
Qy	181	WKSHEGMNLGSNWAYQWVATEGYOSGSNNVTVW 213	
Db	180	WARQGMHLGNNSWYQVATEGYOSGSNNVTVW 212	
OX	RA	Cho S.; Choi Y.;	
NCBI_TaxID=77133;	RA	"Nucleotide sequence analysis of an endo-xylanase gene (xyNA) from	
Q6TLP3_9BACT PRELIMINARY;	RT	Bacillus stearothermophilus.";	
AC	RT	RT	
Q6TLP3;	ID	Bacillus stearothermophilus.	
DT	RA	J. Microbiol. Biotechnol. 5:117-124 (1995).	
05-JUL-2004 (TREMBLrel. 27, Created)	RN		
DT	RA	[2]	
05-JUL-2004 (TREMBLrel. 27, Last sequence update)	RP	SEQUENCE REVISION.	
DT	RA	Cho S.; Choi Y.;	
05-JUL-2004 (TREMBLrel. 27, Last annotation update)	RL	Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.	
DB	CC	-1--CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic	
Endo-1,4-beta-xylanase precursor (EC 3.2.1.8).	CC	linkages in xyans.	
uncultured bacterium.	CC	-1--PATHWAY: Xylan degradation.	
Robertson D.E., Steer B.A.;	CC	-1--SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G) family.	
Bacteria; environmental samples.	CC		
NCBI_TaxID=77133;	CC		
OX	CC		
RP	CC		
Q6TLP3_9BACT PRELIMINARY;	CC		
AC	CC		
Q6TLP3;	CC		
DT	CC		
05-JUL-2004 (TREMBLrel. 27, Created)	CC		
DT	CC		
05-JUL-2004 (TREMBLrel. 27, Last annotation update)	CC		
DB	CC		
Endo-1,4-beta-xylanase precursor (EC 3.2.1.8).	CC		
uncultured bacterium.	CC		
Robertson D.E., Steer B.A.;	CC		
Bacteria; environmental samples.	CC		
NCBI_TaxID=77133;	CC		
OX	CC		
RP	CC		
NUCLEOTIDE SEQUENCE.	CC		
Published=1417865; DOI=10.1101/pS.0333504;	CC		
RX	CC		
Palackal N., Brennan Y., Callien W.N., Dupree P., Frey G., Goubet F.,	CC		
Hazlewood G.P., Healey S., Kang Y.R., Kretz K.A., Lee E., Tan X.,	CC		
Tomlinson G.L., Verruto J., Wong V.W.K., Mathur E.J., Short J.M.,	CC		
Robertson D.E., Steer B.A.;	CC		
"An evolutionary route to xylanase process fitness.";	CC		
Protein Sci. 13:494-503 (2004).	CC		
RL	CC		
EMBL; AY94562; AAO050180.2; -; Genomic_DNA.	CC		
HSSP; P09850; 1BCX.	CC		
SMR; Q6TLP3; 30-214.	CC		
DR	CC		
GO; GO:0031176; P: endo-1,4-beta-xylanase activity; IEA.	CC		
DR	CC		
GO; GO:0005975; P: carbohydrate metabolism; IEA.	CC		
DR	CC		
InterPro; IPR001137; Glyco_hydro_11.	CC		
Pfam; PF00457; Glyco_hydro_11.	CC		
PRINTS; PR00911; GLYDRYLASE1.	CC		
DR	CC		
PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.	CC		
DR	CC		
PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.	CC		
DR	CC		
Glycosidase; Hydrolase; Signal; Xylan degradation.	CC		
PFT	CC		
SIGNAL	CC		
1	CC		

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RESULT 12

XYNA_BACT

STANDARD

PRT; 210 AA.

AC P45705;

DT 01-NOV-1995 (Rel. 32, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (xylanase A) (1..4..

DE Endo-D-xylan xylanohydrolase A).

GN Name=xyNA;

GN Bacteria; Firmicutes; Bacillales; Geobacillus.

GN Bacteria; Firmicutes; Bacillales; Geobacillus.

NCBI_TaxID=1472;

RN NCBITaxonID=1472;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=No. 236;

RA Cho S.; Choi Y.;

RA "Nucleotide sequence analysis of an endo-xylanase gene (xyNA) from Bacillus stearothermophilus.";

RT RT

RN J. Microbiol. Biotechnol. 5:117-124 (1995).

RN [2]

RP SEQUENCE REVISION.

RA Cho S.; Choi Y.;

RA RIL

RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.

CC -1--CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic linkages in xyans.

CC -1--PATHWAY: Xylan degradation.

CC -1--SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G) family.

CC

DR U15985; AAB72117.1; -; Genomic_DNA.

DR HSSP; P09850; 1XNB.

DR SMR; P45705; 24-210.

DR InterPro; IPR001137; Glyco_hydro_11.

DR PFM0457; Glyco_hydro_11.

DR PR00911; GLYDRYLASE1.

DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.

DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.

DR Glycosidase; Hydrolase; Signal; Xylan degradation.

PFT SIGNAL

PT	CHAIN	20	210	Endo-1,4-beta-xylosidase A.
PT	ACT_SITE	104	104	Nucleophile (By similarity).
PT	ACT_SITE	197	197	Proton donor (By similarity).
SQ	SEQUENCE	210 AA;	23221 MW;	3190CF74C34AA845 CRC64;
Query Match		79.4%;	Score 930;	DB 1;
Best Local Similarity	80.6%;	Pred. No. 5.	Length 210;	
Matches	170;	Conservative	11;	Mismatches 28;
				Indels 2;
Qy	3	KEPKRNFLVGLSALMSLFSLSATASAMSTDYQWNTDGGTLYGTRSPLEIYVVDMSGTYRPTGY	62	
Db	2	KUKKRMFLLTLTASMSLGLFGATSSAR-TDWTQYWTDDGGMNAVNGPGGNTSVTWQNTG	60	
Qy	63	NFVVGKGMWTTGSPERTINYNAGWAPNGNGLYTLYGTRSPLEIYVVDMSGTYRPTGY	122	
Db	61	NFVVGKGMWTTGSPERTINYNAGWAPNGNGLYTLYGTRSPLEIYVVDMSGTYRPTGY	120	
Qy	123	KCTVKSDGTYDLYTTRYNASIDGDRTTFQWYSRQSKRPTGSNATITFSNHNAWK	182	
Db	121	KCTVKSDGTYDLYTTRYNASIDGDRTTFQWYSRQSKRPTGSNATITFSNHNAWR	179	
Qy	183	SHGMNLLGSNWAVQVMMATEGYQSSGSNTVW	213	
Db	180	SKGMNLLGSNWAVQVMMATEGYQSSGSNTVW	210	
RESULT 13				
Q43993	AERPU		PRT;	211 AA.
AC	Q43993,_AERPU PRELIMINARY;		PRT;	211 AA.
DT	01-NOV-1996	(TREMBLrel. 01;	Created)	
DT	01-MAR-2004	(TREMBLrel. 26;	Last annotation update)	
GN	Name=xynaA;			
OS	Aeromonas punctata (Aeromonas caviae).			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;			
OX	Aeromonadaceae; Aeromonas.			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=ME-1; TISSUE= Gut content of silk worm;			
RA	Kubota K.B., Suzuki T., Horitsu H., Kawai K., Takamizawa K.,			
RT	"Xylanase I of Aeromonas caviae ME-1 isolated from the intestine of a			
RT	herbivorous insect (Samia cynthia pryeri)." ;			
RL	Biosci. Biotechnol. Biochem. 56:1463-1464(1992).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=ME-1; TISSUE= Gut content of silk worm;			
RA	Kubota K.B., Suzuki T., Horitsu H., Kawai K., Takamizawa K.,			
RA	"Molecular cloning of the xynaA gene encoding an endo-xylosidase (xylosidase I) of Aeromonas caviae ME-1." ;			
RL	Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; D32065; BRA068371; - ; Genomic_DNA.			
HSSP	P09850; 1XNB.			
DR	SMR; Q43993; 25-211.			
DR	GO; GO:000553; P: hydrolyses activity, hydrolyzing O-glycosyl . . . ; IEA.			
DR	GO; GO:0005975; P: carbohydrate metabolism; IEA.			
DR	GO; GO:0045493; P: xylian catabolism; IEA.			
DR	InterPro; IPR001137; Glyco hydro-11.			
DR	Pfam; PF00457; Glyco hydro-11; 1.			
DR	PRINTS; PR00941; GLYCDRASE1.			
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.			
KW	Xylan degradation.			
SQ	SEQUENCE	210 AA;	CRC64;	
Qy			Query Match	73 8%;
Db			Best Local Similarity	74 2%;
			Matches	158;
			Conservative	19;
			Mismatches	33;
			Indels	3;
			Gaps	2;
RESULT 14				
Q713S5	BACFI		PRT;	210 AA.
AC	Q713S5,_BACFI PRELIMINARY;		PRT;	210 AA.
DT	05-JUL-2004	(TREMBLrel. 27;	Created)	
DT	05-JUL-2004	(TREMBLrel. 27;	Last sequence update)	
DT	05-JUL-2004	(TREMBLrel. 27;	Last annotation update)	
DB	DE			
OS	Xylanase.			
OC	Bacillus firmus.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OC	NCBI_TaxID=1399;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=K-1;			
RA	Chuanusumrarn U., Ratanakhanokchai K., Cheevadhanarak S.;			
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF317713; AAQ14588.1; - ; Genomic_DNA.			
DR	HSSP; P09850; 1BCX.			
DR	SMR; Q713S5; 27-210.			
DR	GO; GO:0004553; P: hydrolase activity, hydrolyzing O-glycosyl . . . ; IEA.			
DR	GO; GO:005975; P: carbohydrate metabolism; IEA.			
DR	InterPro; IPR001137; Glyco hydro-11.			
DR	Pfam; PF00457; Glyco hydro-11; 1.			
DR	PRINTS; PR00941; GLYCDRASE1.			
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.			
KW	Xylan degradation.			
SQ	SEQUENCE	210 AA;	CRC64;	
Qy			Query Match	73 8%;
Db			Best Local Similarity	74 2%;
			Matches	158;
			Conservative	19;
			Mismatches	33;
			Indels	3;
			Gaps	2;
RESULT 15				
Q9KEF3	BACHD		PRT;	210 AA.
AC	Q9KEF3,_BACHD PRELIMINARY;		PRT;	210 AA.
DR	01-OCT-2000	(TREMBLrel. 15;	Created)	

01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 13-SPR-2005 (TREMBLrel. 31, Last annotation update)
 DT Endo-1, 4-beta-xylanhydrolyase.
 GN Name=xyn11a; OrderedLocusNames=BH0899;
 OS Bacteriia; halodurans.
 OC Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=86665;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/gar17;
 RA Takami H., Nakase K., Takaki Y., Maeno G., Sasai R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliophilic bacterium *Bacillus*
 halodurans and genomic sequence comparison with *Bacillus subtilis*."
 RT MIR32.
 RT Extremophiles 6:391-395 (2002).
 RL [2]
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX STRAIN=MIR32;
 RA Martinez M.A., Delgado O.D., Breccia J.D., Sineriz F.;
 RL Submitted (Oct-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL:BA00004; BAB18181.; Genomic DNA.
 DR EMBL:AY70624; AAO122761.; Genomic_DNA.
 DR PIR: C83762; CB3762.
 DR HSSP: P09850; 1XNB.
 DR SMR: Q9KEF3; 27-210.
 DR GO: 0016787; :hydrolase activity; IEA.
 DR GO: 0004553; F:carbohydrate activity, hydrolyzing O-glycosyl . . . ; IEA.
 DR GO: 0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR001137; Glyco_hydro_11.
 DR Pfam: PF00457; Glyco_hydro_11.
 DR PRINTS: PRO0911; GHYDRASE1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR Complete proteome; Hydrolase.
 KW Sequence 210 AA; 23313 MW; ACAB5DD5D67A1B2 CRC64;
 SQ TGNFIVKGWTTGSPRTINTAGWAPNGYLTLYGWTSPRLYYVDSMGTYRPTG 120
 Qy 1 MFKFKENLVLGUSAALMSLISFSATAASAASDYNQWTGGIVYNAVNGSGGGNYSVNNWN 60
 Db 1 MFKFVTKVLTIVIAATISFCLSAVPSA - NTYQWQWTGGTIVNATNGGGNISVTWRD 58
 Qy 61 TGNFIVKGWTTGSPRTINTAGWAPNGYLTLYGWTSPRLYYVDSMGTYRPTG 120
 Db 59 TGNFIVKGWTTGSPRTINTAGWAPNGYLTLYGWTSPRLYYVDSMGTYRPTG 118
 Qy 121 TYKGTIVKSDFGTYDITTRYNAPSIDGDRITFTOWSVRSQSKPTGSGNATITFSNHVNA 180
 Db 119 THRGTIVSDGGTYDITTRYNAPSIDGQ-TFQQFWSVRSQSKPTGNNVTSFSNHVNA 177
 Qy 181 WKSHEGMNUGSNWAYQWYMATEGYQSSGSNTVW 213
 Db 178 WRNAGHNLGSWSYQVLTATEQYQSSGRSNTVW 210

GenCore version 5.1.7
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OM protein - protein search, using bw model

Run on: February 3, 2006, 09:11:33 ; Search time 28 Seconds
(without alignments)
628.926 Million cell updates/sec

Title: US-10-626-724-5
Perfect score: 1171
Sequence: 1 MPKFKKNFLVGLSAAALMSIS...YQWMAATEGYQSSGSNSVTVW 213

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:
1: /cgn2_6/pctodata/1/iaa/5_COMB.pep:
2: /cgn2_6/pctodata/1/iaa/6_COMB.pep:
3: /cgn2_6/pctodata/1/iaa/H_COMB.pep:
4: /cgn2_6/pctodata/1/iaa/PCTUS_COMB.pep:
5: /cgn2_6/pctodata/1/iaa/RE_COMB.pep:
6: /cgn2_6/pctodata/1/iaa/backfiles.pep:
*
* No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	116.8	99.7	213	2	US-09-570-856B-1	Sequence 1, Appli
2	116.8	99.7	213	2	US-09-570-856B-13	Sequence 13, Appli
3	114.1	97.4	208	1	US-08-3104-695-21	Sequence 21, Appli
4	113.0	96.5	213	1	US-08-104-445-3	Sequence 3, Appli
5	104.1	88.9	185	1	US-08-044-621D-37	Sequence 37, Appli
6	104.1	88.9	185	1	US-08-709-912-5	Sequence 5, Appli
7	103.8	88.6	185	1	US-09-047-370-5	Sequence 5, Appli
8	103.8	88.6	185	1	US-08-044-621D-36	Sequence 36, Appli
9	103.8	88.6	185	1	US-08-709-912-3	Sequence 3, Appli
10	98.7	88.6	185	1	US-09-047-370-3	Sequence 3, Appli
11	98.7	84.3	185	2	US-09-570-856B-5	Sequence 5, Appli
12	98.4	84.0	185	2	US-09-570-856B-9	Sequence 9, Appli
13	97.9	83.6	185	2	US-09-570-856B-7	Sequence 7, Appli
14	97.7	83.4	185	2	US-09-570-856B-4	Sequence 4, Appli
15	97.6	83.3	185	2	US-09-570-856B-6	Sequence 6, Appli
16	97.4	83.2	185	2	US-09-570-856B-3	Sequence 3, Appli
17	95.5	81.6	185	2	US-09-570-856B-10	Sequence 10, Appli
18	95.5	81.6	211	1	US-08-575-964-1	Sequence 1, Appli
19	95.5	81.6	211	1	US-08-563-500-1	Sequence 1, Appli
20	95.1	81.2	185	2	US-09-570-856B-12	Sequence 12, Appli
21	93.3	79.7	185	2	US-09-570-856B-8	Sequence 8, Appli
22	92.0	78.6	185	2	US-09-570-856B-11	Sequence 11, Appli
23	61.0	54.7	189	1	US-08-709-912-13	Sequence 13, Appli
24	61.0	54.7	189	1	US-09-047-370-13	Sequence 13, Appli
25	63.6	54.4	240	2	US-09-570-856B-16	Sequence 16, Appli
26	63.6	54.3	344	1	US-08-466-812-2	Sequence 2, Appli
27	63.6	54.3	344	2	US-08-590-563-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-570-856B-1
; Sequence 1, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1.RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570, 856B
; PRIORITY FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133, 714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Bacillus circulans
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1) ..(28)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (29) ..()
; OTHER INFORMATION:
; US-09-570-856B-1
Query Match 99.7% ; Score 1168 ; DB 2 ; Length 213 ;
Best Local Similarity 99.5% ; Pred. No. 6.3e-98 ;
Matches 212 ; Conservative 1 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
Qy 1 MFKPKRNFLVGLSAAALMSISLFSRATAASTDYQWNTDGGIVNAVNGSGGNYSYVWSN 60
Db 1 MFKPKRNFLVGLSAAALMSISLFSRATAASTDYQWNTDGGIVNAVNGSGGNYSYVWSN 60
Qy 61 TGNFVFGKGMWTTGSPRTINYAGWAPNGNGYLTYGWRSPRLYYVVDWSGTYRPTG 120
Db 61 TGNFVFGKGMWTTGSPRTINYAGWAPNGNGYLTYGWRSPRLYYVVDWSGTYRPTG 120
Qy 61 TGNFVFGKGMWTTGSPRTINYAGWAPNGNGYLTYGWRSPRLYYVVDWSGTYRPTG 120
Db 121 TYKGTVKSDGTYDLYTTRYNAPSIDGDRRTFTQWYVRSOKRPTGSNATITFSHVNA 180
Db 121 TYKGTVKSDGTYDLYTTRYNAPSIDGDRRTFTQWYVRSOKRPTGSNATITFTHVNA 180
Qy 181 WKSHEGNLGSNWAYQWMAATEGYQSSSSNTVW 213
Db 181 WKSHEGNLGSNWAYQWMAATEGYQSSSSNTVW 213

RESULT 2
 US-09-570-856B-13
 Sequence 13, Application US/09570856B
 Patent No. 6682923
 GENERAL INFORMATION:
 APPLICANT: Bentzien, Joerg M
 TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
 FILE REFERENCE: A-67418-1/BFT/RMS/RMK
 CURRENT APPLICATION NUMBER: US/09/570, 856B
 CURRENT FILING DATE: 2002-04-15
 PRIOR APPLICATION NUMBER: US 60/133, 714
 PRIOR FILING DATE: 1999-05-12
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 13
 LENGTH: 213
 TYPE: PRT
 ORGANISM: *Bacillus subtilis*
 FEATURE:
 NAME/KEY: SIGNAL
 LOCATION: (1) ..(28)
 OTHER INFORMATION:
 FEATURE: mat_peptide
 NAME/KEY: mat_peptide
 LOCATION: (29) ..()
 OTHER INFORMATION:
 US-09-570-856B-13

Query Match 99.7%; Score 1168; DB 2; Length 213;
 Best Local Similarity 99.5%; Pred. No. 6.3e-98;
 Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MFKFKNPLVGLSAALMSISLFSATASAASSTDYQWNWTGGIVNAVNGGGGNTSYVNSWN 60
 Db 1 MFKFKNPLVGLSAALMSISLFSATASAASSTDYQWNWTGGIVNAVNGGGGNTSYVNSWN 60

Qy 61 TGNFVYKGWTTGSPPRTINTNAGWAPNGCYLTYGTRSPLEYYYDWSGTYRPTG 120
 Db 61 TGNFVYKGWTTGSPPRTINTNAGWAPNGCYLTYGTRSPLEYYYDWSGTYRPTG 120

Qy 121 TYKGTVKSDGTYDLYTTTRYNAPSIDGDRTTFQWYSRQSKRTGSNATITFSNHVNA 180
 Db 121 TYKGTVKSDGTYDLYTTTRYNAPSIDGDRTTFQWYSRQSKRTGSNATITFSNHVNA 180

US-08-104-445-3
 Sequence 3, Application 08/104445
 Patent No. 5306633
 GENERAL INFORMATION:
 APPLICANT: GOTTSCHALK, MICHAEL
 APPLICANT: SCHUSTER, ERWIN
 APPLICANT: SPRESSLER, BRUNO
 TITLE OF INVENTION: BACTERIAL XYLANASE, METHOD FOR ITS PRODUCTION
 TITLE OF INVENTION: BACTERIA PRODUCING A XYLANASE, DNA FRAGMENT
 TITLE OF INVENTION: ENCODING A XYLANASE, PLASMID CONTAINING THE DNA FRAGMENT
 TITLE OF INVENTION: BAKING AGENTS CONTAINING A XYLANASE, AND METHOD FOR
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
 STREET: 1755 S. Jefferson Davis Highway, Suite 400
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/104, 445
 FILING DATE:
 CLASSIFICATION: 435

RESULT 3
 US-08-315-695-21
 Sequence 21, Application US/08315695
 Patent No. 5591619
 GENERAL INFORMATION:
 APPLICANT: Li, Xin-Liang
 APPLICANT: Liungdahl, Lars G
 TITLE OF INVENTION: Aureobasidium pullulans Xylanase, Gene
 TITLE OF INVENTION: and Signal Sequence
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 STREET: 5370 Manhattan Circle, Suite 201
 CITY: Boulder
 STATE: CO
 ZIP: 80303
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

TELECOMMUNICATION INFORMATION :
 TELEPHONE: 613-786-0199
 TELEFAX: 613-563-9869
 TELEX:
 INFORMATION FOR SEQ ID NO: 37 :
 SEQUENCE CHARACTERISTICS:
 LENGTH: 185
 TYPE: Amino Acid
 STRANDEDNESS: No. 5405769 Relevant
 TOPOMETRY: Linear
 MOLECULE TYPE:
 DESCRIPTION: protein
 HYPOTHETICAL: No
 ANTI-SENSE: No
 FRAGMENT TYPE: No
 ORIGINAL SOURCE:
 ORGANISM: *Bacillus subtilis*
 IMMEDIATE SOURCE:
 POSITION IN GENOME:
 FEATURE:
 PUBLICATION INFORMATION:
 AUTHORS: Paice M.G., Bourbonnais R
 AUTHORS: M., Jurasek L., & Yaguchi
 TITLE: Arch. Microbiol.
 JOURNAL: Arch. Microbiol.
 VOLUME: 144
 ISSUE:
 PAGES: 201-206
 DATE: 1986
 DOCUMENT NUMBER:
 FILING DATE:
 PUBLICATION DATE:
 RELEVANT RESIDUES IN SEQ ID NO:
 US-08-044-621D-37

Query 29 ASTDTWQWNWTGGGTNVAVNGGAGNYSVNA
 Db 1 ASTDTWQWNWTGGGTNVAVNGGAGNYSVNA

Query 89 NGNGYLTLYGWTRSPLIETYYVDSWGTYY
 Db 61 NGNGYLTLYGWTRSPLIETYYVDSWGTYY

Query 149 DRTTFTQWYVRSQSKRPTGSNATITFSN
 Db 121 DRTTFTQWYVRSQSKRPTGSNATITFSN

Query 209 NVTWV 213
 Db 181 NVTWV 185

RESULT 6
 US-08-709-912-5
 ; Sequence 5, Application US/08709912
 ; Patent No. 579840
 ; GENERAL INFORMATION:
 ; APPLICANT: Sung Dr., Wing L.
 ; APPLICANT: Yaguchi Dr., Kazuhiko
 ; TITLE OF INVENTION: Modification of x
 ; TITLE OF INVENTION: Thermophilicity,
 ; TITLE OF INVENTION: Thermotolerance
 ; NUMBER OF SEQUENCES: 54
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fitzpatrick, Cella, Harpp
 ; STREET: 277 Park Ave.
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States

COUNTRY: USA
 ZIP: 10172-0194
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/709,912
 FILING DATE: 09-SEP-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Olsen Mr., Warren E
 REGISTRATION NUMBER: 27290
 REFERENCE/DOCKET NUMBER: 1039.2000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-2400
 TELEFAX: (212) 758-2982
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 185 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 ORGANISM: *Bacillus subtilis*
 PUBLICATION INFORMATION:
 AUTHORS: Parce, M.G.
 AUTHORS: Bourbonnais, R
 AUTHORS: Desrochers, M
 AUTHORS: Jurasek, L
 AUTHORS: Yaguchi, M
 JOURNAL: Arch. Microbiol.
 VOLUME: 144
 PAGES: 201-206
 DATE: 1986

US-08-709,912-5

Query Match 88.9%; Score 1041; DB 1; Length 185;
 Best Local Similarity 100.0%; Pred. No. 1.6e-86;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 ASTDWNQWTGGTIVNAVNGGGNYSVMSNTGNFVGKWTGSPFRTINTAGWAP 88
 Db 1 ASTDWNQWTGGTIVNAVNGGGNYSVMSNTGNFVGKWTGSPFRTINTAGWAP 60

Qy 89 NGNGVLTLYGWTSPRLJEVYVYDSDNGTYPTGTYKSDGGTYDIYTTTTRYNAPSIDG 148
 Db 61 NGNGVLTLYGWTSPRLJEVYVYDSDNGTYPTGTYKSDGGTYDIYTTTTRYNAPSIDG 120

Qy 149 DRTTQWYTSVQSRPRTGSNATIFSNHNNNAWKGMMNLGSNWAYQVATEGYQSSSS 208
 Db 121 DRTTQWYTSVQSRPRTGSNATIFSNHNNNAWKGMMNLGSNWAYQVATEGYQSSSS 180

Qy 209 NVTW 213
 Db 181 NVTW 185

RESULT 7
 US-09-047-370-5
 Sequence 5, Application US/09047370
 Patent No. 5666408
 GENERAL INFORMATION:
 APPLICANT: Sung Dr., Wing L
 APPLICANT: Yaguchi Dr., Makoto
 APPLICANT: Ishikawa Dr., Kazuhiko
 TITLE OF INVENTION: Modification of Xylanase to Improve
 TITLE OF INVENTION: Thermophilicity, Alkalophilicity and

TITLE OF INVENTION: Thermostability
 NUMBER OF SEQUENCES: 54
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Fitpatrick, Cella, Harper, and Scinto
 STREET: 277 Park Ave.
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10172-0194
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/047,370
 FILING DATE: 09-047,370
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/709,912
 FILING DATE: 09-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Olsen Mr., Warren E
 REGISTRATION NUMBER: 27290
 REFERENCE/DOCKET NUMBER: 1039.2.000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-2400
 TELEFAX: (212) 758-2982
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 185 amino acids
 TYPE: protein
 HYPOTHETICAL: NO
 ANTI SENSE: NO
 FRAGMENT TYPE: internal
 ORIGIN: *Bacillus subtilis*
 PUBLICATION INFORMATION:
 AUTHORS: Parce, M.G.
 AUTHORS: Bourbonnais, R
 AUTHORS: Desrochers, M
 AUTHORS: Jurasek, L
 AUTHORS: Yaguchi, M
 JOURNAL: Arch. Microbiol.
 VOLUME: 144
 PAGES: 201-206
 DATE: 1986

US-09-047-370-5

Query Match 88.9%; Score 1041; DB 1; Length 185;
 Best Local Similarity 100.0%; Pred. No. 1.6e-86;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 ASTDWNQWTGGTIVNAVNGGGNYSVMSNTGNFVGKWTGSPFRTINTAGWAP 88
 Db 1 ASTDWNQWTGGTIVNAVNGGGNYSVMSNTGNFVGKWTGSPFRTINTAGWAP 60

Qy 89 NGNGVLTLYGWTSPRLJEVYVYDSDNGTYPTGTYKSDGGTYDIYTTTTRYNAPSIDG 148
 Db 61 NGNGVLTLYGWTSPRLJEVYVYDSDNGTYPTGTYKSDGGTYDIYTTTTRYNAPSIDG 120

Qy 89 NGNGVLTLYGWTSPRLJEVYVYDSDNGTYPTGTYKSDGGTYDIYTTTTRYNAPSIDG 148
 Db 61 NGNGVLTLYGWTSPRLJEVYVYDSDNGTYPTGTYKSDGGTYDIYTTTTRYNAPSIDG 120

Qy 149 DRTTQWYTSVQSRPRTGSNATIFSNHNNNAWKGMMNLGSNWAYQVATEGYQSSSS 208
 Db 121 DRTTQWYTSVQSRPRTGSNATIFSNHNNNAWKGMMNLGSNWAYQVATEGYQSSSS 180

Qy 209 NVTW 213
 Db 181 NVTW 185

RESULT 7
 US-09-047-370-5
 Sequence 5, Application US/09047370
 Patent No. 5666408
 GENERAL INFORMATION:
 APPLICANT: Sung Dr., Wing L
 APPLICANT: Yaguchi Dr., Makoto
 APPLICANT: Ishikawa Dr., Kazuhiko
 TITLE OF INVENTION: Modification of Xylanase to Improve
 TITLE OF INVENTION: Thermophilicity, Alkalophilicity and

RESULT 8
 US-08-044-621D-16
 / Sequence 36, Application US/08044621D
 / Patent No. 540769
 / GENERAL INFORMATION:
 / APPLICANT: Warren W. Wakarchuk
 / APPLICANT: Wing L. Sung
 / APPLICANT: Makoto Yaguchi
 / APPLICANT: Robert L. Campbell
 / APPLICANT: David R. Rose
 / TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
 / TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
 / NUMBER OF SEQUENCES: 37
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Gowing, Strathy & Henderson
 / STREET: Suite 2600, 160 Elgin Street
 / STATE: Ontario
 / COUNTRY: Canada
 / ZIP: K1P 1C3
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette, 5.25 in., 360kB storage
 / COMPUTER: IBM PC
 / OPERATING SYSTEM: PC-DOS
 / SOFTWARE: WordPerfect 5.1
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/044,621D
 / FILING DATE: April 8, 1993
 / CLASSIFICATION: 435
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER:
 / FILING DATE:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Judy A. Erratt
 / REGISTRATION NUMBER: 34,076
 / REFERENCE/DOCKET NUMBER: 08-863796
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 613-736-0199
 / TELEFAX: 613-563-9869
 / TELEX:
 / INFORMATION FOR SEQ ID NO: 36:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 185
 / TYPE: Amino Acid
 / STRANDEDNESS: No. 5405769 Relevant
 / TOPOLOGY: linear
 / MOLECULE TYPE:
 / DESCRIPTION: protein
 / HYPOTHETICAL: No
 / ANTI-SENSE: No
 / FRAGMENT TYPE: No
 / ORIGINAL SOURCE:
 / ORGANISM: *Bacillus circulans*
 / IMMEDIATE SOURCE:
 / POSITION IN GENOME:
 / FEATURE:
 / PUBLICATION INFORMATION:
 / AUTHORS: Yang R.C.A., MacKenzie C.R. & Narang
 / R.A.
 / TITLE:
 / JOURNAL: Nucleic Acids Res.
 / VOLUME: 16
 / ISSUE:
 / PAGES: 7187
 / DATE: 1988
 / DOCUMENT NUMBER:
 / FILING DATE:
 / PUBLICATION DATE:
 / RELEVANT RESIDUES IN SEQ ID NO:
 / US-08-044-621D-36
 / Query Match Score 1038; DB 1; Length 185;
 / Best Local Similarity 99.5%; Pred. No. 3e-86;
 / PAGES: 7187

Matches 184; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 29 ASTDQWNWTGGGIVNAVNGGGTGSVNSNTGIVVGGWTTSSPRTINYAGVWAP 88
 Db 1 ASTDQWNWTGGGIVNAVNGGGTGSVNSNTGIVVGGWTTSSPRTINYAGVWAP 60
 Qy 89 NGNGHTLYGWTSPLEYYVVDSGTYPRTGTYKGTVKSDGGTIDYTTRNAPSIDG 148
 Db 61 NGNGHTLYGWTSPLEYYVVDSGTYPRTGTYKGTVKSDGGTIDYTTRNAPSIDG 120
 Qy 149 DRTTTOYWSVROSQRTGTSNATITFSNHNAWKSQHGMNLGSNWAYQVMATEGYQSGSS 208
 Db 121 DRTTTOYWSVROSQRTGTSNATITFSNHNAWKSQHGMNLGSNWAYQVMATEGYQSGSS 180
 Qy 209 NVTW 213
 Db 181 NVTW 185

RESULT 9
 US-08-709-912-3
 / Sequence 3, Application US/08709912
 / Patent No. 5759840
 / GENERAL INFORMATION:
 / APPLICANT: Sung Dr., Wing L.
 / APPLICANT: Yaguchi Dr., Makoto
 / APPLICANT: Isikawa Dr., Kazuhiko
 / TITLE OF INVENTION: Modification of Xylanase to Improve
 / Thermophilicity, Alkalophilicity and
 / Thermostability
 / NUMBER OF SEQUENCES: 54
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
 / STREET: 277 Park Ave.
 / CITY: New York
 / STATE: New York
 / COUNTRY: USA
 / ZIP: 10172-0194
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC DOS/MS-DOS
 / SOFTWARE: Patentin Release #1.1, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/709,912
 / FILING DATE: 09-SEP-1996
 / CLASSIFICATION: 435
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Olsen Mr., Warren E.
 / REGISTRATION NUMBER: 27290
 / REFERENCE/DOCKET NUMBER: 1039.2000
 / APPLICATION NUMBER: US/08/709,912
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (212) 758-2400
 / TELEFAX: (212) 758-2882
 / INFORMATION FOR SEQ ID NO: 3:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 185 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / HYPOTHETICAL: NO
 / ANTI-SENSE: NO
 / FRAGMENT TYPE:
 / ORIGINAL SOURCE:
 / ORGANISM: *Bacillus circulans*
 / IMMEDIATE SOURCE:
 / POSITION IN GENOME:
 / FEATURE:
 / PUBLICATION INFORMATION:
 / AUTHORS: Yang R.C.A., MacKenzie C.R. & Narang
 / R.A.
 / TITLE:
 / JOURNAL: Nucleic Acids Res.
 / VOLUME:
 / ISSUE:
 / PAGES: 7187
 / DATE: 1988
 / DOCUMENT NUMBER:
 / FILING DATE:
 / PUBLICATION DATE:
 / RELEVANT RESIDUES IN SEQ ID NO:
 / US-08-044-621D-36
 / Query Match Score 1038; DB 1; Length 185;
 / Best Local Similarity 99.5%; Pred. No. 3e-86;
 / PAGES: 7187

DATE: 1988
US-08-709-912-3

Query Match 88.6%; Score 1038; DB 1; Length 185;
Best Local Similarity 99.5%; Pred. No. 3e-86; Indels 0; Gaps 0;
Matches 184; Conservative 1; N mismatches 0;

Qy 29 ASTDWNWTGGIVNAVNGGGNNYSVNWNTGNFVVKGWTGSPFRTINTNAGWAP 88
Db 1 ASTDWNWTGGIVNAVNGGGNNYSVNWNTGNFVVKGWTGSPFRTINTNAGWAP 60

Qy 89 NGNGYLTLIGWTRSPLEYVVDNGTYPKGTVKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NGNGYLTLIGWTRSPLEYVVDNGTYPKGTVKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFQWVSYRQSKRPTGSNATITFSNHYNAWKSHGMLGNSWYQVNAMEGYQSSGS 208
Db 121 DRTTFQWVSYRQSKRPTGSNATITFTNHNWNAWKSHGMLGNSWYQVNAMEGYQSSGS 180

Qy 209 NVTW 213
Db 181 NVTW 185

RESULT 10
US-09-047-370-3

Patent No. 5866408

SEQUENCE 3, Application US/09047370
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
STREET: Fitzpatrick, Cella, Harper, and Scinto
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOSS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr., Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039-2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2932
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:

ORGANISM: Bacillus circulans
PUBLICATION INFORMATION:
AUTHORS: Yang, R.C.A.
AUTHORS: Mackenzie, C.R.
AUTHORS: Narang, S.A.
JOURNAL: Nucleic Acid Research
VOLUME: 16
PAGES: 7187
DATE: 1988
US-09-047-370-3

Query Match 88.6%; Score 1038; DB 1; Length 185;
Best Local Similarity 99.5%; Pred. No. 3e-86; Indels 0; Gaps 0;
Matches 184; Conservative 1; N mismatches 0;

Qy 29 ASTDWNWTGGIVNAVNGGGNNYSVNWNTGNFVVKGWTGSPFRTINTNAGWAP 88
Db 1 ASTDWNWTGGIVNAVNGGGNNYSVNWNTGNFVVKGWTGSPFRTINTNAGWAP 60

Qy 89 NGNGYLTLIGWTRSPLEYVVDNGTYPKGTVKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NGNGYLTLIGWTRSPLEYVVDNGTYPKGTVKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFQWVSYRQSKRPTGSNATITFSNHYNAWKSHGMLGNSWYQVNAMEGYQSSGS 208
Db 121 DRTTFQWVSYRQSKRPTGSNATITFTNHNWNAWKSHGMLGNSWYQVNAMEGYQSSGS 180

RESULT 11
US-09-570-856B-5

Sequence 5, Application US/09570856B
Patent No. 668293

GENERAL INFORMATION:
APPLICANT: Bentzien, Joerg M
APPLICANT: Dahiyat, Bassil I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-6748-/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT FILING DATE: 2002-04-15
PRIORITY APPLICATION NUMBER: US 60/133,714
PRIORITY FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 185
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic

US-09-570-856B-5

Query Match 84.3%; Score 987; DB 2; Length 185;
Best Local Similarity 94.6%; Pred. No. 1.e-81; Indels 0; Gaps 0;

Qy 29 ASTDWNWTGGIVNAVNGGGNNYSVNWNTGNFVVKGWTGSPFRTINTNAGWAP 88
Db 1 ASTDWNWTGGIVNAVNGGGNNYSVNWNTGNFVVKGWTGSPFRTINTNAGWAP 60

Qy 89 NGNGYLTLIGWTRSPLEYVVDNGTYPKGTVKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NGNGYLTLIGWTRSPLEYVVDNGTYPKGTVKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFQWVSYRQSKRPTGSNATITFSNHYNAWKSHGMLGNSWYQVNAMEGYQSSGS 208
Db 121 DRTTFQWVSYRQSKRPTGSNATITFTNHNWNAWKSHGMLGNSWYQVNAMEGYQSSGS 180

Qy 209 NVTW 213
Db 181 NVTW 185

Db 181 NVTW 185

RESULT 12
 US-09-570-856B-9
 ; Sequence 9, Application US/09570856B
 ; Patent No. 6662923
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentzien, Joerg M
 ; APPLICANT: Dahiyat, Bassil I
 ; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
 ; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
 ; CURRENT APPLICATION NUMBER: US/09/570, 856B
 ; CURRENT FILING DATE: 2002-04-15
 ; PRIOR APPLICATION NUMBER: US 60/133, 714
 ; PRIOR FILING DATE: 1999-05-12
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 9
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE: OTHER INFORMATION: synthetic
 ; OTHER INFORMATION: synthetic

US-09-570-856B-9

Query Match 84.0%; Score 984; DB 2; Length 185;
 Best Local Similarity 93.5%; Pred. No. 2.3e-81; Indels 0; Gaps 0;
 Matches 173; Conservative 6; Mismatches 6;

Db 1 ASTDWNWTDGGIVNAVNGGGNTSVNWSNTGNFVGKWTGSPRTINYAGWAP 88
 1 ASTDWNWTDGGIVNAVNGGGNTSVNWSNTGNFVGKWTGSPRTINYAGWAP 60

Db 29 ASTDWNWTDGGIVNAVNGGGNTSVNWSNTGNFVGKWTGSPRTINYAGWAP 88
 1 ASTDWNWTDGGIVNAVNGGGNTSVNWSNTGNFVGKWTGSPRTINYAGWAP 60

Db 89 NGNGYLTLYGWTRSPLEYYVDSMGTGTYKPTGTVKSDGGTYDIYTTTRNAPSIDG 148
 61 NGNGYLTLYGWTRSPLEYYVDSMGTGTYKPTGTVKSDGGTYDIYTTTRNAPSIDG 120

Db 149 DRTTFTQWYSVRSQSKRTGSNATITFSNHNAWKSQHGMNLGSNWAYQVMATEGYQSSGS 208
 121 DRTTFTQWYSVRSQSKRTGSNATITFSNHNAWKSQHGMNLGSNWAYQVMATEGYQSSGS 180

Db 209 NVTW 213
 181 NVTW 185

RESULT 13
 US-09-570-856B-7
 ; Sequence 7, Application US/09570856B
 ; Patent No. 6662923
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentzien, Joerg M
 ; APPLICANT: Dahiyat, Bassil I
 ; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
 ; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
 ; CURRENT APPLICATION NUMBER: US/09/570, 856B
 ; CURRENT FILING DATE: 2002-04-15
 ; PRIOR APPLICATION NUMBER: US 60/133, 714
 ; PRIOR FILING DATE: 1999-05-12
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 7
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE: OTHER INFORMATION: synthetic

US-09-570-856B-7

Query Match 83.6%; Score 979; DB 2; Length 185;
 Best Local Similarity 94.1%; Pred. No. 6.5e-81; Indels 0; Gaps 0;
 Matches 174; Conservative 6; Mismatches 6;

Query Match 83.4%; Score 977; DB 2; Length 185;
 Best Local Similarity 94.1%; Pred. No. 9.8e-81; Indels 0; Gaps 0;
 Matches 174; Conservative 5; Mismatches 6;

Db 29 ASTDWNWTDGGIVNAVNGGGNTSVNWSNTGNFVGKWTGSPRTINYAGWAP 88
 1 ASTDWNWTDGGIVNAVNGGGNTSVNWSNTGNFVGKWTGSPRTINYAGWAP 60

Db 89 NGNGYLTLYGWTRSPLEYYVDSMGTGTYKPTGTVKSDGGTYDIYTTTRNAPSIDG 148
 61 NGNGYLTLYGWTRSPLEYYVDSMGTGTYKPTGTVKSDGGTYDIYTTTRNAPSIDG 120

Db 149 DRTTFTQWYSVRSQSKRTGSNATITFSNHNAWKSQHGMNLGSNWAYQVMATEGYQSSGS 208
 121 DRTTFTQWYSVRSQSKRTGSNATITFSNHNAWKSQHGMNLGSNWAYQVMATEGYQSSGS 180

Db 209 NVTW 213
 181 NVTW 185

RESULT 14
 US-09-570-856B-4
 ; Sequence 4, Application US/09570856B
 ; Patent No. 6682923
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentzien, Joerg M
 ; APPLICANT: Dahiyat, Bassil I
 ; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
 ; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
 ; CURRENT APPLICATION NUMBER: US/09/570, 856B
 ; CURRENT FILING DATE: 2002-04-15
 ; PRIOR APPLICATION NUMBER: US 60/133, 714
 ; PRIOR FILING DATE: 1999-05-12
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 4
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic

US-09-570-856B-4

Query Match 83.4%; Score 977; DB 2; Length 185;
 Best Local Similarity 94.1%; Pred. No. 9.8e-81; Indels 0; Gaps 0;

Query Match 83.4%; Score 977; DB 2; Length 185;
 Best Local Similarity 94.1%; Pred. No. 9.8e-81; Indels 0; Gaps 0;

Db 29 ASTDWNWTDGGIVNAVNGGGNTSVNWSNTGNFVGKWTGSPRTINYAGWAP 88
 1 ASTDWNWTDGGIVNAVNGGGNTSVNWSNTGNFVGKWTGSPRTINYAGWAP 60

Db 89 NGNGYLTLYGWTRSPLEYYVDSMGTGTYKPTGTVKSDGGTYDIYTTTRNAPSIDG 148
 61 NGNGYLTLYGWTRSPLEYYVDSMGTGTYKPTGTVKSDGGTYDIYTTTRNAPSIDG 120

Db 149 DRTTFTQWYSVRSQSKRTGSNATITFSNHNAWKSQHGMNLGSNWAYQVMATEGYQSSGS 208
 121 DRTTFTQWYSVRSQSKRTGSNATITFSNHNAWKSQHGMNLGSNWAYQVMATEGYQSSGS 180

Db 209 NVTW 213
 181 NVTW 185

RESULT 15
 US-09-570-856B-6
 ; Sequence 6, Application US/09570856B
 ; Patent No. 6682923
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentzien, Joerg M
 ; APPLICANT: Dahiyat, Bassil I
 ; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
 ; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
 ; CURRENT APPLICATION NUMBER: US/09/570, 856B
 ; CURRENT FILING DATE: 2002-04-15

PRIOR APPLICATION NUMBER: US 60/133,714
PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 185
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: synthetic
US-09-570-856B-6

	Query	Match	Score	DB	Length
	Best Local Similarity	83.3%	976	2	185
Matches	174; Conservative	94.1%	Pred. No.	1.2e-80;	
		5;	Ms.matches	6;	Indels
					0;
Qy	29 ASTDWNQWTGGGIVNAVNGGGNYSVNRNTGNFVVKGWTGSPPTINNAGVWAP 88				
Db	1 ASTDWNQWTGGGIVNAVNGGGNYSVNRNTGNFVVKGWTGSPPTINNAGVWAP 60				
Qy	89 NGNGYLTLIGKTRSPLEYVVDISGTYRPTGTYKGTGTVKGDGGTIDIVYTTTRNAPSING 148				
Db	61 NGNGYLTLIGKTRSPLEYVVDISGTYRPTGTYKGTGTVKGDGGTIDIVYTTTRNAPSING 120				
Qy	149 DRTTFIQWYSYRQSKRPTGSNATITFSNHYNAWIKSHGMNLGSNAYQVNTATEGYQSSGS 208				
Db	121 DRTTFIQWYSYRQSKRPTGSNATITFSNHYNAWIKSHGMNLGSNAYQVNTATEGYQSSGS 180				
Qy	209 NVTW 213				
Db	181 NVTW 185				

Search completed: February 3, 2006, 09:12:10
Job time : 29 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	1171	100.0	213	6 US-10-517-939-188	Sequence 188, App
2	1171	100.0	213	7 US-11-170-633-16	Sequence 16, App
3	1168	99.7	213	6 US-10-517-939-224	Sequence 224, App
4	1168	99.7	213	7 US-11-170-633-17	Sequence 17, App
5	1104	94.3	213	6 US-10-517-939-230	Sequence 230, App
6	1097	93.7	213	6 US-10-517-939-302	Sequence 302, App
7	1041	88.9	185	7 US-11-170-633-1	Sequence 1, App
8	953	81.4	211	6 US-10-517-939-198	Sequence 198, App
9	933.5	79.7	214	6 US-10-517-939-158	Sequence 158, App
10	929	79.3	211	7 US-11-170-633-19	Sequence 19, App
11	927	79.2	210	6 US-10-517-939-208	Sequence 208, App
12	907.5	77.5	211	7 US-11-170-633-18	Sequence 18, App
13	886	75.7	189	6 US-10-517-939-190	Sequence 190, App
14	873.5	74.6	184	6 US-10-517-939-252	Sequence 252, App
15	844	72.1	189	6 US-10-517-939-380	Sequence 380, App
16	834	71.2	189	6 US-10-517-939-378	Sequence 378, App
17	826	70.5	189	6 US-10-517-939-376	Sequence 376, App
18	710	60.6	222	6 US-10-517-939-168	Sequence 168, App
19	687	58.7	445	6 US-10-517-939-368	Sequence 368, App
20	669	57.2	225	6 US-10-517-939-172	Sequence 172, App
21	663.5	56.7	241	7 US-11-170-633-43	Sequence 43, App
22	659	56.3	240	7 US-11-170-633-42	Sequence 42, App
23	658	56.3	361	6 US-10-517-939-212	Sequence 212, App
24	647.5	55.3	355	6 US-10-517-939-206	Sequence 206, App
25	646	55.2	242	7 US-11-170-633-41	Sequence 41, App

Db 121 TYKGTVKSDGCTDYIYTTRYNAPSIDGDRTTFTQYWSURQSKRPTGSNATITFSNHVNA 180
 Qy 181 WKSHEGNLNLGSNWAYQWMAATEGYQSSGSSNTVW 213
 Db 181 WKSHEGNLNLGSNWAYQWMAATEGYQSSGSSNTVW 213

RESULT 2

US-11-170-653-16
 Sequence 16, Application US/11170653
 Publication No. US20050271769A1
 GENERAL INFORMATION:
 APPLICANT: Danisco A/S
 APPLICANT: Sibbesen, Ole
 APPLICANT: Sorensen, Jens
 TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
 FILE REFERENCE: 674509-2046
 CURRENT APPLICATION NUMBER: US/11/170, 653
 CURRENT FILING DATE: 2005-06-23
 PRIOR APPLICATION NUMBER: US/10/237, 386
 PRIOR FILING DATE: 2002-09-09
 PRIOR APPLICATION NUMBER: PCT/IB01/00426
 PRIOR FILING DATE: 2001-03-08
 PRIOR APPLICATION NUMBER: GB 0005585.5
 PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: GB 0015751.1
 PRIOR FILING DATE: 2000-06-27
 NUMBER OF SEQ ID NOS: 66
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 16
 LENGTH: 213
 TYPE: PRT
 ORGANISM: *Bacillus subtilis*
 US-11-170-653-16

Query Match 100.0%; Score 1171; DB 7; Length 213;
 Best Local Similarity 100.0%; Pred. No. 7.6e-96;
 Mismatches 0; Indels 0; Gaps 0;

RESULT 4

US-11-170-653-17
 Sequence 17, Application US/11170653
 Publication No. US20050271769A1
 GENERAL INFORMATION:
 APPLICANT: Sofsensen, Jens
 APPLICANT: Danisco A/S
 APPLICANT: Sibbesen, Ole
 APPLICANT: Sofsensen, Jens
 TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
 FILE REFERENCE: 674509-2046
 CURRENT APPLICATION NUMBER: US/11/170, 653
 CURRENT FILING DATE: 2005-06-23
 PRIOR APPLICATION NUMBER: GB 0005585.5
 PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: GB 0015751.1
 PRIOR FILING DATE: 2000-06-27
 PRIOR APPLICATION NUMBER: GB 0005585.5
 PRIOR FILING DATE: 2001-03-08
 SEQ ID NO 17
 LENGTH: 213
 TYPE: PRT
 ORGANISM: *Bacillus circulans*
 US-11-170-653-17

RESULT 3

US-10-517-939-224
 Sequence 224, Application US/10517939
 Publication No. US20060003433A1
 GENERAL INFORMATION:
 APPLICANT: Steer, Brian
 APPLICANT: Callen, Walter
 APPLICANT: Healey, Shaun
 APPLICANT: Blum, David
 APPLICANT: Estephania, Alireza
 APPLICANT: Hazlewood, Geoff
 APPLICANT: Blum, David
 APPLICANT: Hazlewood, Geoff
 TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
 FILE REFERENCE: 564462007901
 CURRENT APPLICATION NUMBER: US/10/517, 939
 CURRENT FILING DATE: 2004-12-13

Db 121 TYKGTVKSDGCTDYIYTTRYNAPSIDGDRTTFTQYWSURQSKRPTGSNATITFSNHVNA 180
 Qy 181 WKSHEGNLNLGSNWAYQWMAATEGYQSSGSSNTVW 213
 Db 181 WKSHEGNLNLGSNWAYQWMAATEGYQSSGSSNTVW 213
 Software: FastSEQ for Windows Version 4.0
 SEQ ID NO 224
 LENGTH: 213
 TYPE: PRT
 ORGANISM: Unknown
 FEATURE:
 OTHER INFORMATION: Obtained from an environmental sample
 FEATURE:
 NAME/KEY: SIGNAL
 LOCATION: (1)...(28)
 US-10-517-939-224
 Query Match 99.7%; Score 1168; DB 6; Length 213;
 Best Local Similarity 99.5%; Pred. No. 1.4e-95;
 Mismatches 0; Indels 0; Gaps 0;
 Matches 212; Conservative 1;
 Qy 1 MFKEFKNLFVGLSALMSISLFSATASAATDYNQWTDGGGIVNAVNGGGNYSVNWSN 60
 Db 1 MFKEFKNLFVGLSALMSISLFSATASAATDYNQWTDGGGIVNAVNGGGNYSVNWSN 60
 Qy 61 TGNFVFGKGMGTGSFERTINYAGWAPNGYLTLYGTRSPLEYYVDSMGTYRPTG 120
 Db 61 TGNFVFGKGMGTGSFERTINYAGWAPNGYLTLYGTRSPLEYYVDSMGTYRPTG 120
 Qy 121 TYKGTVKSDGCTDYIYTTRYNAPSIDGDRTTFTQYWSURQSKRPTGSNATITFSNHVNA 180
 Db 121 TYKGTVKSDGCTDYIYTTRYNAPSIDGDRTTFTQYWSURQSKRPTGSNATITFSNHVNA 180
 Qy 181 WKSHEGNLNLGSNWAYQWMAATEGYQSSGSSNTVW 213
 Db 181 WKSHEGNLNLGSNWAYQWMAATEGYQSSGSSNTVW 213
 Software: FastSEQ for Windows Version 4.0
 SEQ ID NO 224
 LENGTH: 213
 TYPE: PRT
 ORGANISM: Unknown
 FEATURE:
 OTHER INFORMATION: Obtained from an environmental sample
 FEATURE:
 NAME/KEY: SIGNAL
 LOCATION: (1)...(28)
 US-10-517-939-224
 Query Match 99.7%; Score 1168; DB 6; Length 213;
 Best Local Similarity 99.5%; Pred. No. 1.4e-95;
 Mismatches 0; Indels 0; Gaps 0;
 Matches 212; Conservative 1;
 Qy 1 MFKEFKNLFVGLSALMSISLFSATASAATDYNQWTDGGGIVNAVNGGGNYSVNWSN 60
 Db 1 MFKEFKNLFVGLSALMSISLFSATASAATDYNQWTDGGGIVNAVNGGGNYSVNWSN 60

RESULT 5

US-10-517-939-230

Sequence 230, Application US/10517939

Publication No. US20060003433A1

GENERAL INFORMATION:

APPLICANT: Steer, Brian

APPLICANT: Callen, Walter

APPLICANT: Healey, Shaun

APPLICANT: Hazlewood, Geoff

APPLICANT: Wu, Di

APPLICANT: Blum, David

APPLICANT: Esteghlalian, Alireza

TITLE OF INVENTION: XYLANASES, NUCLEAR ACIDS ENCODING THEM

FILE REFERENCE: 564462007301

CURRENT APPLICATION NUMBER: US/10/517,939

CURRENT FILING DATE: 2004-12-13

PRIOR APPLICATION NUMBER: PCT/US03/19153

PRIOR FILING DATE: 2003-06-16

PRIOR PUBLISHING DATE: 2003-07-01

NUMBER OF SEQ ID NOS: 380

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 230

LENGTH: 213

TYPE: PRT

ORGANISM: Unknown

FEATURE: Obtained from an environmental sample.

OTHER INFORMATION:

NAME/KEY: SIGNAL

LOCATION: (1) ... (28)

US-10-517-939-302

Query Match 93.7%; Score 1097; DB 6; Length 213;

Best Local Similarity 92.0%; Pred. No. 2.3e-89; Mismatches 7; Indels 0; Gaps 0;

Matches 196; Conservative 10; Mi.matches 7; Indels 0; Gaps 0;

Qy 1 MFKEPKKFLYGLSALMSISLFSATASAASSTDYQWNTDGGIVNAVNGGGNTSYVNSWN 60

Db 1 MFKEPKKFLYGLTAALMSISLFSANASANTDYNWTDGGIVNAVNGGGNTSYVNSWN 60

Qy 61 TGNFVYKGKMTGSPRTINYNAGWAPNGNYLTLYGATRSPLIEYYVDSWGTYRPTG 120

Db 61 TGNFVYKGKMTGSPRTINYNAGWAPNGNYLTLYGATRSPLIEYYVDSWGTYRPTG 120

Qy 121 TYKGTYSKDGTYDYYTTRYNAPSIDGDRITFTQWSVROSKRPTGSNATIFSNHVA 180

Db 121 TYKGTYSKDGTYDVTTRDAPSIDGDKITFTQWSVROSKRPTGSNATIFSNHVA 180

Qy 181 WKSHGMNLGSNWYQMATCQYQSSGSSNTVW 213

Db 181 WKRYGMNLGSNWSYQLTATEQYQSSGSSNTVW 213

RESULT 6

US-10-517-939-302

Sequence 302, Application US/10517939

Publication No. US20060003433A1

GENERAL INFORMATION:

APPLICANT: Steer, Brian

APPLICANT: Callen, Walter

APPLICANT: Healey, Shaun

APPLICANT: Hazlewood, Geoff

APPLICANT: Wu, Di

APPLICANT: Blum, David

APPLICANT: Esteghlalian, Alireza

TITLE OF INVENTION: XYLANASES, NUCLEAR ACIDS ENCODING THEM

FILE REFERENCE: 564462007301

CURRENT APPLICATION NUMBER: US/10/517,939

CURRENT FILING DATE: 2004-12-13

PRIOR APPLICATION NUMBER: PCT/US03/19153

PRIOR FILING DATE: 2003-06-16

PRIOR PUBLISHING DATE: 2003-07-01

NUMBER OF SEQ ID NOS: 380

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 230

LENGTH: 213

TYPE: PRT

ORGANISM: Unknown

FEATURE: Obtained from an environmental sample.

OTHER INFORMATION:

NAME/KEY: SIGNAL

LOCATION: (1) ... (28)

US-10-517-939-230

Query Match 94.3%; Score 1104; DB 6; Length 213;

Best Local Similarity 93.0%; Pred. No. 5.5e-90; Mismatches 8; Indels 0; Gaps 0;

Matches 198; Conservative 10; Mi.matches 8; Indels 0; Gaps 0;

RESULT 7

US-11-170-653-1

Sequence 1, Application US/11170653

Publication No. US200502271769A1

GENERAL INFORMATION:

APPLICANT: Danisco A/S

APPLICANT: Sørensen, Ole

APPLICANT: Sørensen, Ole

TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor

FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/11/170,653

CURRENT FILING DATE: 2005-06-23

PRIOR APPLICATION NUMBER: US/10/237,386

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: GB 0005585,5

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: GB 0015751,1

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 66

SOFTWARE: Patentin version 3.0

FILE REFERENCE: 674509-2046
 CURRENT APPLICATION NUMBER: US/11/170, 653
 CURRENT FILING DATE: 2005-06-23
 PRIORITY NUMBER: US/10/237, 386
 PRIOR FILING DATE: 2002-09-09
 PRIORITY NUMBER: PCT/IB01/00426
 PRIOR FILING DATE: 2001-03-08
 PRIORITY NUMBER: GB 0005585, 5
 PRIOR FILING DATE: 2000-03-08
 PRIORITY NUMBER: GB 0015751, 1
 PRIOR FILING DATE: 2000-06-27
 NUMBER OF SEQ ID NOS: 66
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 19
 LENGTH: 211
 TYPE: PRT
 ORGANISM: A. caviae
 US-11-170-653-19

Query Match 79.2%; Score 927; DB 6; Length 210;
 Best Local Similarity 80.1%; Pred. No. 1.7e-74;
 Matches 169; Conservative 14; Mismatches 26; Indels 2; Gaps 2;

Query Match 79.3%; Score 929; DB 7; Length 211;
 Best Local Similarity 79.3%; Pred. No. 1.1e-74;
 Matches 169; Conservative 18; Mismatches 24; Indels 2; Gaps 2;

RESULT 12
 US-11-170-653-18
 Query 1 MFKPKKNFLVGLSAALMSISLFSATASAASDYYQWNTDGGIVNAVNGGGNYSVWN 60
 Db 1 MFKFGKLLMTVLAASMSFGVFAATSSA-TDYYQWNTDGGGTNAVNGGGNYSVWN 59
 Query 61 TGNFVFGKGWTTGSPRTINTNAGWAPNGCYLTLYGWTRSPLIEYYVDSWGTGTRPG 120
 Db 60 TGNFVFGKGWTTGTPRVRVNTNAGVFAPSGNGYLTYGWTRNALIYYVDSWGTGTRPG 119
 Query 121 TYKGTYSKSDGTYD1YTTTRYNAPSIDGDRTFTQWVSRQSKRPTGSNATITFSNHVNA 180
 Db 120 TYKGTYSNDSGTYD1YTTMRNAPSIDGTTQ-TFQWVSRQSKRPTGVSNTITFSNHVNA 178
 Query 181 WSKGNLGSNWAYQWVQMATGYQSSSSNTVW 213
 Db 179 WPSKGMYLGNWSYQWVQMATGYQSSNANTVW 211

RESULT 11
 US-10-517-939-208
 Sequence 208, Application US/10517939
 Publication No. US20060003433A1
 GENERAL INFORMATION:
 APPLICANT: Steer, Brian
 APPLICANT: Callen, Walter
 APPLICANT: Healey, Shaun
 APPLICANT: Hazelwood, Geoff
 APPLICANT: Wu, Di
 APPLICANT: Blum, David
 APPLICANT: Esteghlalian, Alireza
 TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
 TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
 FILE REFERENCE: 56446207901
 CURRENT APPLICATION NUMBER: US/10/517, 939
 CURRENT FILING DATE: 2004-12-13
 PRIOR APPLICATION NUMBER: PCT/US03/19153
 PRIOR FILING DATE: 2003-06-16
 PRIOR APPLICATION NUMBER: 60/389, 299
 PRIOR FILING DATE: 2002-06-14
 NUMBER OF SEQ ID NOS: 380
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 208
 LENGTH: 210
 TYPE: PRT
 ORGANISM: Unknown
 OTHER INFORMATION: Obtained from an environmental sample
 FEATURE:
 NAME/KEY: SIGNAL
 LOCATION: (1) ... (27)
 US-10-517-939-208

Query Match 79.2%; Score 927; DB 6; Length 210;
 Best Local Similarity 80.1%; Pred. No. 1.7e-74;
 Matches 169; Conservative 14; Mismatches 26; Indels 2; Gaps 2;

Query 3 KPKKNFLVGLSAALMSISLFSATASAASDYYQWNTDGGIVNAVNGGGNYSVWN 62
 Db 2 KLKRMKMLTLLTASMSFGVFAATSSA-TDYYQWNTDGGGTNAVNGGGNYSVWN 60
 Query 63 NFVFGKGWTTGSPRTINTNAGWAPNGCYLTLYGWTRSPLIEYYVDSWGTGTRPG 122
 Db 61 NFVFGKGWTTGSPNVTNAGVFAPSGNGYLTYGWTRNALIYYVDSWGTGTRPG 120
 Query 123 KGTYSKSDGTYD1YTTTRYNAPSIDGDRTFTQWVSRQSKRPTGSNATITFSNHVNA 182
 Db 121 KGTYSNDSGTYD1YTTMRNAPSIDGTTQ-TFQWVSRQSKRPTGVSNTITFSNHVNA 179
 Query 183 WSKGNLGSNWAYQWVQMATGYQSSSSNTVW 213
 Db 180 WPSKGMYLGNWSYQWVQMATGYQSSNANTVW 210

RESULT 13
 US-10-517-939-190

Query Match 77.5%; Score 907.5; DB 7; Length 211;
 Best Local Similarity 79.2%; Pred. No. 8.6e-73;
 Matches 168; Conservative 12; Mismatches 29; Indels 3; Gaps 3;

Query 3 KPKKNFLVGLSAALMSISLFSATASAASDYYQWNTDGGIVNAVNGGGNYSVWN 62
 Db 2 KLKRMKMLTLLTASMSFGVFAATSSA-TDYYQWNTDGGGMVNAVNGPGNYSVWN 60
 Query 63 NFVFGKGWTTGSPRTINTNAGWAPNGCYLTLYGWTRSPLIEYYVDSWGTGTRPG 122
 Db 61 NFVFGKGWTTGSPNVTNAGVFAPSGNGYLTYGWTRNALIYYVDSWGTGTRPG 120
 Query 123 KGTYSKSDGTYD1YTTTRYNAPSIDGDRTFTQWVSRQSKRPTGSNATITFSNHVNA 181
 Db 121 ESGTYSNDSGTYD1YTTMRNAPSIDGTTQ-TFQWVSRQSKRPTGVSNTITFSNHVNA 179
 Query 182 WSKGNLGSNWAYQWVQMATGYQSSSSNTVW 213
 Db 180 WPSKGMYLGNWSYQWVQMATGYQSSNANTVW 211

Db 122 IDGNNTTPTQFMISVRQSKRPIGTNNITPSNHNAWKSKGMLGSSWSYQVLATESYQSS 181
Qy 206 GSSNVTW 213
Db 182 GYSNVTW 189

Search completed: February 3, 2006, 09:13:20
Job time: 8 SECS

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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:12:23 ; Search time 79 Seconds
(without alignments)

1126.552 Million cell updates/sec

Title: US-10-626-724-5

Perfect score: 1171

Sequence: 1 MFKFKNFKFLVGLSAALMSI.....YQVMATEGYQSSGSSNVTWV 213

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:*

1: /cgn2_6/ptodata/1/pubpa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1171	100.0	213	4	US-10-237-386-16	Sequence 16, Appl
2	1171	100.0	213	5	US-10-626-583-5	Sequence 5, Appl
3	1171	100.0	213	5	US-10-626-724-5	Sequence 5, Appl
4	1168	99.7	213	4	US-10-237-386-17	Sequence 17, Appl
5	1161	99.1	213	5	US-10-626-583-11	Sequence 11, Appl
6	1161	99.1	213	5	US-10-626-724-11	Sequence 11, Appl
7	1154	98.5	213	5	US-10-626-583-7	Sequence 7, Appl
8	1154	98.5	213	5	US-10-626-724-7	Sequence 7, Appl
9	1149	98.1	213	5	US-10-626-583-9	Sequence 9, Appl
10	1149	98.1	213	5	US-10-626-724-9	Sequence 9, Appl
11	1130	96.5	213	5	US-10-626-583-3	Sequence 3, Appl
12	1130	96.5	213	5	US-10-626-724-3	Sequence 3, Appl
13	1041	88.9	185	6	US-10-307-441-5	Sequence 5, Appl
14	1041	88.9	185	4	US-10-237-386-1	Sequence 1, Appl
15	1041	88.9	185	6	US-11-088-725A-32	Sequence 32, Appl
16	1041	88.9	197	4	US-10-442-148A-10	Sequence 10, Appl
17	1041	88.9	360	4	US-10-442-148A-11	Sequence 11, Appl
18	1038	88.6	185	6	US-10-307-441-3	Sequence 3, Appl
19	1038	88.6	185	6	US-11-088-725A-30	Sequence 30, Appl
20	929	79.3	211	4	US-10-237-386-19	Sequence 19, Appl
21	907.5	77.5	211	4	US-10-237-386-18	Sequence 18, Appl
22	885	75.6	185	6	US-11-018-645-2	Sequence 2, Appl
23	885	75.6	186	6	US-11-018-645-14	Sequence 14, Appl
24	826.5	70.6	192	6	US-11-018-645-8	Sequence 8, Appl
25	825	70.5	186	6	US-11-018-645-16	Sequence 16, Appl
26	686.5	58.6	197	6	US-11-018-645-4	Sequence 4, Appl
27	686.5	58.6	198	6	US-11-018-645-18	Sequence 18, Appl

RESULT 1
US-10-237-386-16
; Sequence 16, Application US-10237386
; Publication No. US2003180885AI
; GENERAL INFORMATION:
; APPLICANT: Daniasco A/S
; APPLICANT: Sibbesen, Ole
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674503-2046
; CURRENT APPLICATION NUMBER: US-10-237-386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 66
; SEQ ID NO 16
; SOFTWARE: Patentin version 3.0
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-237-386-16

Query Match 100.0%; Score 1171; DB 4; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKEFKNFKLGSALMSIISLFSATASAASSTDYQWNTDGGIVNAVNGSGGNYSYNWSN 60
Db 1 MFKEFKNFKLGSALMSIISLFSATASAASSTDYQWNTDGGIVNAVNGSGGNYSYNWSN 60

Qy 61 TGNFVKGKWTGSPRTINYAGTWAPNGGYLTYGWRSPRLYYVDSWKGTRPTG 120
Db 61 TGNFVKGKWTGSPRTINYAGTWAPNGGYLTYGWRSPRLYYVDSWKGTRPTG 120

Qy 121 TYKGTVKSDGTYDLYTTRYNAPSIDGDRITIPTQWYSRQSKRTGSNATITFSNHVNA 180
Db 121 TYKGTVKSDGTYDLYTTRYNAPSIDGDRITIPTQWYSRQSKRTGSNATITFSNHVNA 180

Qy 181 WKSHEGMNLGSNWAYQVMATEGYQSSGSSNTVW 213
Db 181 WKSHEGMNLGSNWAYQVMATEGYQSSGSSNTVW 213

Qy 181 WKSHEGMNLGSNWAYQVMATEGYQSSGSSNTVW 213
Db 181 WKSHEGMNLGSNWAYQVMATEGYQSSGSSNTVW 213

RESULT 2
US-10-626-583-5
; Sequence 5, Application US-10626583

Publication No. US20040234998A1

GENERAL INFORMATION:

APPLICANT: SIBBESSEN, OLE

TITLE OF INVENTION: PROTEINS

FILE REFERENCE: 07883/0132

CURRENT APPLICATION NUMBER: US/10/626,583

CURRENT FILING DATE: 2003-07-25

PRIOR APPLICATION NUMBER: US/09/869,155

PRIOR FILING DATE: 2001-10-01

PRIOR APPLICATION NUMBER: PCT/IB99/02071

PRIOR FILING DATE: 1999-12-17

PRIOR APPLICATION NUMBER: GB 9828599.2

PRIOR FILING DATE: 1998-12-23

PRIOR APPLICATION NUMBER: GB 9807805.7

PRIOR FILING DATE: 1999-04-06

PRIOR APPLICATION NUMBER: GB 9908645.6

PRIOR FILING DATE: 1999-04-15

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 5

LENGTH: 213

TYPE: PRT

ORGANISM: *Bacillus subtilis*

US-10-626-583-5

Query Match 100.0%; Score 1171; DB 5; Length 213;
 Best Local Similarity 100.0%; Pred. No. 1.5e-96;
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKEKRNFLVGLSALMSISLFSATASASTDYNQWNTDGGG1IVNAYNGGGNYSVNNEN 60
 Db 1 MFKEKRNFLVGLSALMSISLFSATASASTDYNQWNTDGGG1IVNAYNGGGNYSVNNEN 60

Qy 61 TGNFVKGKMTGSFERTINYNAQWAPNGNGYLTYGWTSPLEIYVVDMSGTYRPTG 120
 Db 61 TGNFVKGKMTGSFERTINYNAQWAPNGNGYLTYGWTSPLEIYVVDMSGTYRPTG 120

Qy 121 TYKGTVKSDGCTDYYTTRYNAPSIDGRTTFTQYWSVRQSRTGSNATITFSNHVNA 180
 Db 121 TYKGTVKSDGCTDYYTTRYNAPSIDGRTTFTQYWSVRQSRTGSNATITFSNHVNA 180

Qy 181 WKSHEMNLLGSNWAYQVMATEGYQSSGSSNTVW 213
 Db 181 WKSHEMNLLGSNWAYQVMATEGYQSSGSSNTVW 213

RESULT 3
 US-10-626-724-5
 Sequence 5, Application US/10626724
 GENERAL INFORMATION:
 APPLICANT: SIBBESSEN, OLE
 TITLE OF INVENTION: PROTEINS
 FILE REFERENCE: 07883/0132
 CURRENT APPLICATION NUMBER: US/10/626,724
 CURRENT FILING DATE: 2003-07-25
 PRIOR APPLICATION NUMBER: US/09/869,155
 PRIOR FILING DATE: 2001-06-25
 PRIOR APPLICATION NUMBER: PCT/IB99/02071
 PRIOR FILING DATE: 1999-12-17
 PRIOR APPLICATION NUMBER: GB 9828599.2
 PRIOR FILING DATE: 1998-12-23
 PRIOR APPLICATION NUMBER: GB 9807805.7
 PRIOR FILING DATE: 1999-04-06
 PRIOR APPLICATION NUMBER: GB 9908645.6
 PRIOR FILING DATE: 1999-04-15
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 5
 LENGTH: 213
 TYPE: PRT

RESULT 5
 US-10-626-583-11

RESULT 4
 US-10-237-386-17
 Sequence 17, Application US/10237386
 Publication No. US20030180895A1
 GENERAL INFORMATION:
 APPLICANT: Sibbesen, Ole
 APPLICANT: Sørensen, Jens
 TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
 FILE REFERENCE: 674509-20416
 CURRENT APPLICATION NUMBER: US/10/237,386
 CURRENT FILING DATE: 2002-12-06
 PRIOR APPLICATION NUMBER: PCT/IB01/00426
 PRIOR FILING DATE: 2001-03-08
 PRIOR APPLICATION NUMBER: GB 0005585.5
 PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: GB 0015751.1
 NUMBER OF SEQ ID NOS: 66
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 17
 LENGTH: 213
 TYPE: PRT
 ORGANISM: *Bacillus circulans*
 US-10-237-386-17

Query Match 99.7%; Score 1168; DB 4; Length 213;
 Best Local Similarity 99.5%; Pred. No. 2.8e-96;
 Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKEKRNFLVGLSALMSISLFSATASASTDYNQWNTDGGG1IVNAYNGGGNYSVNNEN 60
 Db 1 MFKEKRNFLVGLSALMSISLFSATASASTDYNQWNTDGGG1IVNAYNGGGNYSVNNEN 60

Qy 61 TGNFVKGKMTGSFERTINYNAQWAPNGNGYLTYGWTSPLEIYVVDMSGTYRPTG 120
 Db 61 TGNFVKGKMTGSFERTINYNAQWAPNGNGYLTYGWTSPLEIYVVDMSGTYRPTG 120

Qy 121 TYKGTVKSDGCTDYYTTRYNAPSIDGRTTFTQYWSVRQSRTGSNATITFSNHVNA 180
 Db 121 TYKGTVKSDGCTDYYTTRYNAPSIDGRTTFTQYWSVRQSRTGSNATITFSNHVNA 180

Qy 181 WKSHEMNLLGSNWAYQVMATEGYQSSGSSNTVW 213
 Db 181 WKSHEMNLLGSNWAYQVMATEGYQSSGSSNTVW 213

RESULT 5
 US-10-626-583-11

Sequence 11, Application US/10626583
 Publication No. US200402349988.1
 GENERAL INFORMATION:
 APPLICANT: SIBBESSEN, OLE
 TITLE OF INVENTION: PROTEINS
 FILE REFERENCE: 078883/0132
 CURRENT APPLICATION NUMBER: US/10/626,583
 CURRENT FILING DATE: 2003-07-25
 PRIORITY APPLICATION NUMBER: US/09/869,155
 PRIORITY FILING DATE: 2001-10-01
 PRIORITY APPLICATION NUMBER: PCT/IB99/02071
 PRIORITY APPLICATION NUMBER: GB 9907805.7
 PRIORITY FILING DATE: 1999-04-06
 PRIORITY APPLICATION NUMBER: GB 9908645.6
 PRIORITY FILING DATE: 1999-04-15
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 11
 LENGTH: 213
 TYPE: PRT
 FEATURE: Artificial Sequence
 ORGANISM: Mutant xylanase
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Mutant xylanase
 US-10-626-583-11

Query Match 99.1%; Score 1161; DB 5; Length 213;

Best Local Similarity 99.1%; Pred. No. 1.2e-35; Indels 0; Gaps 0;
 Matches 211; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFKPKKNFLVGLSAALMSISLFSATASAASSTDYQWNTDGGTIVNAVNGSGCGNYSYNWSN 60
 Db 1 MFKPKKNFLVGLSAALMSISLFSATASAASSTDYQWNTDGGTIVNAVNGSGCGNYSYNWSN 60
 Qy 61 TGNFVYKGWTTGSPPRTINTNAGVWAPNGCYLTYGWRSPLEYYVDSWGTYRPTG 120
 Db 61 TGNFVYKGWTTGSPPRTINTNAGVWAPNGCYLTYGWRSPLEYYVDSWGTYRPTG 120
 Qy 121 TYKGTVRSDDGTYDIYTTTRNAPSIDGDRTTFTQWSVRSKRPTGSNATITFSNHVNA 180
 Db 121 TYKGTVRSDDGTYDIYTTTRNAPSIDGDRTTFTQWSVRSKRPTGSNATITFSNHVNA 180
 Qy 181 WKSHEGMNLGSNWAYQVMATEGYQSSSSNTVW 213
 Db 181 WKSHEGMNLGSNWAYQVMATEGYQSSSSNTVW 213

RESULT 7
 US-10-626-583-7

Sequence 7, Application US/10626583
 Publication No. US200402349988A1
 GENERAL INFORMATION:
 APPLICANT: SIBBESSEN, OLE
 TITLE OF INVENTION: PROTEINS
 FILE REFERENCE: 078883/0132
 CURRENT APPLICATION NUMBER: US/10/626,583
 CURRENT FILING DATE: 2003-07-25
 PRIORITY APPLICATION NUMBER: US/09/869,155
 PRIORITY FILING DATE: 2001-10-01
 PRIOR APPLICATION NUMBER: PCT/IB99/02071
 PRIOR FILING DATE: 1999-12-17
 PRIOR APPLICATION NUMBER: GB 9828599.2
 PRIOR FILING DATE: 1998-12-23
 PRIOR APPLICATION NUMBER: GB 9907805.7
 PRIOR FILING DATE: 1999-04-06
 PRIOR APPLICATION NUMBER: GB 9908645.6
 PRIOR FILING DATE: 1999-04-15
 NUMBER OF SEQ ID NOS: 19
 SEQ ID NO: 7
 LENGTH: 213
 TYPE: PRT
 FEATURE: Artificial Sequence
 ORGANISM: Mutant xylanase
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-10-626-583-7

RESULT 6
 US-10-626-724-11
 Sequence 11, Application US/10626724
 Publication No. US20050079573A1
 GENERAL INFORMATION:
 APPLICANT: SIBBESSEN, OLE
 TITLE OF INVENTION: PROTEINS
 FILE REFERENCE: 078883/0132
 CURRENT APPLICATION NUMBER: US/10/626,724
 PRIORITY APPLICATION NUMBER: US/09/869,155
 PRIORITY FILING DATE: 2003-07-25
 PRIORITY APPLICATION NUMBER: PCT/IB99/02071
 PRIORITY FILING DATE: 1999-12-17
 PRIORITY APPLICATION NUMBER: GB 9828599.2
 PRIORITY FILING DATE: 1998-12-23
 PRIORITY APPLICATION NUMBER: GB 9907805.7
 PRIORITY FILING DATE: 1999-04-06
 PRIORITY APPLICATION NUMBER: GB 9908645.6
 NUMBER OF SEQ ID NOS: 19

Query Match 98.5%; Score 1154; DB 5; Length 213;

Best Local Similarity 98.1%; Pred. No. 4.9e-95; Indels 0; Gaps 0;
 Matches 209; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 MFKPKKNFLVGLSAALMSISLFSATASAASSTDYQWNTDGGTIVNAVNGSGCGNYSYNWSN 60
 Db 1 MFKPKKNFLVGLSAALMSISLFSATASAASSTDYQWNTDGGTIVNAVNGSGCGNYSYNWSN 60
 Qy 61 TGNFVYKGWTTGSPPRTINTNAGVWAPNGCYLTYGWRSPLEYYVDSWGTYRPTG 120

; OTHER INFORMATION: Mutant Xylanase
us-10-626-724-9

Query Match 98.1%; Score 1149; DB 5; Length 213;
Best Local Similarity 97.7%; Pred. No. 1. 4e-34;
Matches 208; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MPFKKRNFLVGLSAALMSISLFSATASAASDYYWQWTGCGIIVNAVNGSGCGNSYVNSN 60
Db 1 MPFKKRNFLVGLSAALMSISLFSATASAASDYYWQWTGCGIIVNAVNGSGCGNSYVNSN 60
Qy 61 TGNFVVKGWTGSPPTINTAGWAPNGCYLTYGWTSPLEYYVDSWGTYRPTG 120
Db 61 TGNFVVKGWTGSPPTINTAGWAPNGCYLTYGWTSPLEYYVDSWGTYRPTG 120
Qy 121 TYKGTVKSDGGTYDIYTTRYNAPSIDGDRTFTQWSVRSKRPTGSNATITFSNHVNA 180
Db 121 TYKGTVKSDGGTYDIYTTRYNAPSIDGDRTFTQWSVRSKRPTGSNATITFSNHVNA 180
Qy 181 WKSHEGNLGSWAYQMATEGYQSSGSSNVTVW 213
Db 181 WKSHEGNLGSWAYQMATEGYQSSGSSNVTVW 213

RESULT 11
US-10-626-583-3
; Sequence 3, Application US/10626583
; Publication No. US20040234998A1
; GENERAL INFORMATION
; APPLICANT: SIBBESSEN, OLE
; APPLICANT: SORENSEN, JENS FRISBAEK
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; PRIOR FILING DATE: 1999-04-15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Xylanase
US-10-626-724-3

Query Match 96.5%; Score 1130; DB 5; Length 213;
Best Local Similarity 95.3%; Pred. No. 6.9e-93;
Matches 203; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
Qy 1 MPFKKRNFLVGLSAALMSISLFSATASAASDYYWQWTGCGIIVNAVNGSGCGNSYVNSN 60
Db 1 MPFKKRNFLVGLTAAMFSISMSATASAAGDYYWQWTGCGIIVNAVNGSGCGNSYVNSN 60
Qy 61 TGNFVVKGWTGSPPTINTAGWAPNGCYLTYGWTSPLEYYVDSWGTYRPTG 120
Db 61 TGNFVVKGWTGSPPTINTAGWAPNGCYLTYGWTSPLEYYVDSWGTYRPTG 120
Qy 121 TYKGTVKSDGGTYDIYTTRYNAPSIDGDRTFTQWSVRSKRPTGSNATITFSNHVNA 180
Db 121 TYKGTVKSDGGTYDIYTTRYNAPSIDGDRTFTQWSVRSKRPTGSNATITFSNHVNA 180
Qy 181 WKSHEGNLGSWAYQMATEGYQSSGSSNVTVW 213
Db 181 WKSHEGNLGSWAYQMATEGYQSSGSSNVTVW 213

RESULT 13
US-10-307-441-5
; Sequence 5, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION
; APPLICANT: SUNG, Wing L.
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
; FILE REFERENCE: 027367-5006US
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; OTHER INFORMATION: Description of Unknown Organism: Xylanase
us-10-626-583-3

Query Match 96.5%; Score 1130; DB 5; Length 213;
Best Local Similarity 95.3%; Pred. No. 6.9e-93;
Matches 203; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
Qy 1 MPFKKRNFLVGLSAALMSISLFSATASAASDYYWQWTGCGIIVNAVNGSGCGNSYVNSN 60
Db 1 MPFKKRNFLVGLTAAMFSISMSATASAAGDYYWQWTGCGIIVNAVNGSGCGNSYVNSN 60
Qy 61 TGNFVVKGWTGSPPTINTAGWAPNGCYLTYGWTSPLEYYVDSWGTYRPTG 120
Db 61 TGNFVVKGWTGSPPTINTAGWAPNGCYLTYGWTSPLEYYVDSWGTYRPTG 120
Qy 121 TYKGTVKSDGGTYDIYTTRYNAPSIDGDRTFTQWSVRSKRPTGSNATITFSNHVNA 180
Db 121 TYKGTVKSDGGTYDIYTTRYNAPSIDGDRTFTQWSVRSKRPTGSNATITFSNHVNA 180
Qy 181 WKSHEGNLGSWAYQMATEGYQSSGSSNVTVW 213

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; SEQ ID NO 5
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-307-441-5

Query Match 88.9%; Score 1041; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 5.3e-85;
Matches 185; Conservative 0; N mismatches 0; Indels 0; Gaps 0;
Db 1 ASTDWNQNTDGGIIVNAVNGSGNNYSVNSNTGNFVKGWTGSPFRTINTNAGWWAP 60
Db 1 ASTDWNQNTDGGIIVNAVNGSGNNYSVNSNTGNFVKGWTGSPFRTINTNAGWWAP 60

Query 29 NGNGYLTLGWTSPLEYYVDSMGTYRPTGTVKSDGTYDIYTTTRYNAPSIDG 148
Db 61 NGNGYLTLGWTSPLEYYVDSMGTYRPTGTVKSDGTYDIYTTTRYNAPSIDG 120
Db 149 DRTTFTQWVSYVQSKRPTGSNATITFSNHYNAWKSHGMNLGSNWAYQVNAATEGYQSSGS 208
Db 121 DRTTFTQWVSYVQSKRPTGSNATITFSNHYNAWKSHGMNLGSNWAYQVNAATEGYQSSGS 180
Db 181 NVTWV 213
Db 181 NVTWV 185

Query 209 NVTWV 213
Db 181 NVTWV 185

Query Match 88.9%; Score 1041; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 5.3e-85;
Matches 185; Conservative 0; N mismatches 0; Indels 0; Gaps 0;
Db 1 ASTDWNQNTDGGIIVNAVNGSGNNYSVNSNTGNFVKGWTGSPFRTINTNAGWWAP 88
Db 1 ASTDWNQNTDGGIIVNAVNGSGNNYSVNSNTGNFVKGWTGSPFRTINTNAGWWAP 60

Query 29 ASTDWNQNTDGGIIVNAVNGSGNNYSVNSNTGNFVKGWTGSPFRTINTNAGWWAP 88
Db 1 ASTDWNQNTDGGIIVNAVNGSGNNYSVNSNTGNFVKGWTGSPFRTINTNAGWWAP 60

Query 89 NGNGYLTLGWTSPLEYYVDSMGTYRPTGTVKSDGTYDIYTTTRYNAPSIDG 148
Db 61 NGNGYLTLGWTSPLEYYVDSMGTYRPTGTVKSDGTYDIYTTTRYNAPSIDG 120

Query 89 NGNGYLTLGWTSPLEYYVDSMGTYRPTGTVKSDGTYDIYTTTRYNAPSIDG 148
Db 149 DRTTFTQWVSYVQSKRPTGSNATITFSNHYNAWKSHGMNLGSNWAYQVNAATEGYQSSGS 208
Db 121 DRTTFTQWVSYVQSKRPTGSNATITFSNHYNAWKSHGMNLGSNWAYQVNAATEGYQSSGS 180
Db 181 NVTWV 213
Db 181 NVTWV 185

Search completed: February 3, 2006, 09:13:51
Job time : 80 secs

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; SEQ ID NO 1
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-237-386-1

Query Match 88.9%; Score 1041; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 5.3e-85;
Matches 185; Conservative 0; N mismatches 0; Indels 0; Gaps 0;
Db 1 ASTDWNQNTDGGIIVNAVNGSGNNYSVNSNTGNFVKGWTGSPFRTINTNAGWWAP 88
Db 1 ASTDWNQNTDGGIIVNAVNGSGNNYSVNSNTGNFVKGWTGSPFRTINTNAGWWAP 60

Query 29 ASTDWNQNTDGGIIVNAVNGSGNNYSVNSNTGNFVKGWTGSPFRTINTNAGWWAP 88
Db 1 ASTDWNQNTDGGIIVNAVNGSGNNYSVNSNTGNFVKGWTGSPFRTINTNAGWWAP 60

Query 89 NGNGYLTLGWTSPLEYYVDSMGTYRPTGTVKSDGTYDIYTTTRYNAPSIDG 148
Db 61 NGNGYLTLGWTSPLEYYVDSMGTYRPTGTVKSDGTYDIYTTTRYNAPSIDG 120
Db 149 DRTTFTQWVSYVQSKRPTGSNATITFSNHYNAWKSHGMNLGSNWAYQVNAATEGYQSSGS 208
Db 121 DRTTFTQWVSYVQSKRPTGSNATITFSNHYNAWKSHGMNLGSNWAYQVNAATEGYQSSGS 180
Db 181 NVTWV 213
Db 181 NVTWV 185

Search completed: February 3, 2006, 09:13:51
Job time : 80 secs

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